

REMARKS

Attached hereto is a marked up version of the changes made to the specification by this amendment. The attachment is captioned “**Version With Markings to Show Changes Made.**”

Reconsideration and withdrawal of the rejections of this application and consideration and entry of this paper are respectfully requested in view of the herein remarks and accompanying information, which place the application in condition for allowance.

I. STATUS OF CLAIMS AND FORMAL MATTERS

Claims 1-25 are pending. Claims 1-25 are amended without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents.

No new matter is added. Support for the amended claims is found throughout the specification.

It is submitted that these claims are patentably distinct from the references cited by the Examiner, and that these claims are in full compliance with the requirements of 35 U.S.C. §112. The amendments of the claims herein are not made for the purpose of patentability within the meaning of 35 U.S.C. §§ 101, 102, 103 or 112; but rather the amendments are made simply for clarification and to round out the scope of protection to which Applicants are entitled.

II. RESPONSE TO RESTRICTION REQUIREMENT

The March 30, 2001 Office Action required an election under 35 U.S.C. § 121 and 37 CFR 1.141 from among:

Group I. SEQ ID NOs 1 and 7;

Group II. SEQ ID NOs 2 and 8;

Group III. SEQ ID NOs 3 and 9;

Group IV. SEQ ID NOs 4 and 10;

Group V. SEQ ID NOs 5 and 11; and

Group VI. SEQ ID NOs 6 and 12.

Pursuant to the telephone conversation of February 20, 2001 with Examiner Souaya, the election of Group I, SEQ ID NOs 1 and 7, with traverse, is affirmed. Reconsideration and withdrawal of the restriction requirement are respectfully requested in view of the remarks herewith.

As a traverse, it is noted that the MPEP lists two criteria for a proper restriction requirement. First, the inventions must be independent or distinct. MPEP § 803. Second, searching the additional inventions must constitute an undue burden on the examiner if restriction is not required. *Id.* The MPEP directs the examiner to search and examine an entire application “[i]f the search and examination of an entire application can be made without serious burden, ...even though it includes claims to distinct or independent inventions.” *Id.*

The amino acid sequences (SEQ ID NOs 1-6) and the nucleic acids encoding them (SEQ ID NOs 7-12) are drawn functionally to the same enzyme, a glucan lyase. Furthermore, the invention is drawn to a process of producing an anti-oxidant *in situ*, in which process, preferably, an α -1,4-glucan lyase is used. The sequences 1-6 are given as six possible α -1,4-glucan lyases, as mere examples. Thus, each sequence does not constitute a separate invention, as the invention is the process of producing an anti-oxidant *in situ* from a glucan substrate.

In addition, it is respectfully submitted that a search of all of the related nucleotide and amino acid sequences presented in this application also does not pose a serious burden to the examiner. For example, as shown by the enclosed comparison, the peptides represented by SEQ ID NOs 2, 5 and 6 and the corresponding nucleic acids of SEQ ID NOs 8, 11 and 12 share greater than 74% sequence homology to SEQ ID NOs 1 and 7 respectively, underscoring the interrelated nature of these molecules. It would be unduly burdensome on the Applicants to have to file divisional applications to each amino acid sequence and corresponding nucleotide sequence, particularly as a “broad” process claim is sought.

Therefore, Groups I, II, III, IV, V and VI can be searched and examined in this application as there is no undue or serious burden in searching and examining these claims together. Thus, the restriction requirement is improper; and, it is respectfully requested that the restriction requirement be reconsidered and withdrawn.

III. THE REJECTION UNDER §101 IS OVERCOME

Claims 19-25 stand rejected under 35 U.S.C. §101 as allegedly not reciting any steps involved in the process. The rejection is respectfully traversed. The amendment herein has placed these claims in condition for allowance, rendering the rejection moot. Simply, the “use” recitation is no longer in the claims. Consequently, reconsideration and withdrawal of the rejection is respectfully requested.

IV. THE REJECTION UNDER §112, FIRST PARAGRAPH, IS OVERCOME

Claims 1-18 stand rejected under 35 U.S.C. §112, first paragraph, as allegedly containing non-enabling subject matter. The Office Action contends that the application fails to teach the method of the claimed invention with regard to any recombinant enzyme expressed in any plant to produce any anti-oxidant from a glucan substrate. Applicants disagree. The instant invention is clearly enabled because a skilled artisan would readily understand how to make and use the invention. Further, possession of the invention at the time of filing did exist.

According to the Court of Appeals for the Federal Circuit in the case of *In re Wands*, 8 U.S.P.Q. 2d 1400 (Fed. Cir. 1988),

Enablement is not precluded by the necessity for some experimentation such as routine screening. However, experimentation needed to practice the invention must not be undue experimentation. 'The key word is undue, not experimentation.' The determination of what constitutes undue experimentation in a given case requires the application of standard of reasonableness, having due regard for the nature of the invention and the state of the art. The test is not merely quantitative, since a considerable amount of experimentation is permissible, if it is merely routine, or if the specification in question provides a reasonable amount of guidance with respect to the direction in which the experimentation should proceed ... [Citations omitted].

Id. at 1404.

Against this background, determining whether undue experimentation is required to practice a claimed invention turns on weighing many factors summarized in *In re Wands*, 858 F.2d 731, 8 USPQ2d 1400 (Fed. Cir. 1988) For example, (1) the quantity of experimentation necessary; (2) the amount of direction or guidance presented; (3) the presence or absence of working examples of the invention; (4) the nature of the invention; (5) the state of the prior art; (6) the relative skill of those in the art; (7) the predictability or unpredictability of the art; and (8) the breadth of the claims.

Thus, the assertion in the Office Action that the instant invention does not provide enablement for expressing any recombinant enzyme in any plant to produce any anti-oxidant from a glucan substrate is misplaced because undue experimentation would not exist. Applying *Wands* to the instant facts, it is clear that enablement exists, to wit, *inter alia*, that the quantity of experimentation necessary is low; the amount of direction or guidance presented is high;

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enabled

working examples are clearly present; the relative skill of those in the art is high; and the predictability of the art is also high.

A skilled artisan would readily understand that a variety of recombinant enzymes which act on a glucan substrate, such as starch, to produce an anti-oxidant, such as anhydrofructose, are known in the art. For example, the enzyme amyloglucoside can act on a glucan substrate to produce glucose, which is then further converted to the anti-oxidant ascorbic acid, for example by glucose oxidase. Thus, it would be unduly restrictive to limit the invention to either a specific enzyme and/or to a specific anti-oxidant.

In addition, several plants, namely grape, potatoes, maize and guar, are, in fact, exemplified (see pages 23-31 of the published PCT specification). It is hereby asserted that the present invention does disclose the invention in a manner which is clear and concise and which would enable a skilled person to carry out the invention.

Thus, it is respectfully submitted that the assertion in the Office Action that the claims are not enabled is obviated. Consequently, the Section 112, first paragraph, rejection should be reconsidered and withdrawn; and, such relief is respectfully requested.

V. THE REJECTION UNDER §112, SECOND PARAGRAPH, IS OVERCOME

Claims 1 and 17-25 stand rejected under 35 U.S.C. §112, second paragraph, as allegedly being indefinite. The amendments submitted herewith place the claims in condition for allowance and have rendered the Section 112, second paragraph, rejection moot. Simply, the bases for the rejection no longer appear in the claims. Consequently, reconsideration and withdrawal of the rejection is believed to be in order and such action is respectfully requested.

VI. THE REJECTION UNDER §103 IS OVERCOME

Claims 1-18 stand rejected under 35 U.S.C. 103(a) as allegedly being unpatentable over Yu(a) or Yu(b) in view of Poulsen and Ishida et al. and Perl et al. The cited documents fail to disclose, suggest, or motivate a skilled artisan to practice, the presently claimed invention. The rejection is respectfully traversed.

The present invention relates to advantageous procedures based on the recombinant expression of glucan-metabolising enzymes in plants to produce anti-oxidants *in situ*.

One aspect of the present invention is based on a strategy of producing, in a medium, anti-oxidants which are metabolites of glucan by expressing within a plant, or part thereof, a

recombinant enzyme which acts on a glucan substrate present within the medium (including the plant or part thereof) to yield the anti-oxidant. This is in direct contrast to previously known procedures for producing glucan metabolite anti-oxidants which either rely on the addition of purified enzymes to a glucan-containing medium or use microorganisms expressing the enzymes.

In another aspect of the present invention, anti-oxidants are produced *in situ* in plants transformed with enzymes that convert glucans to anti-oxidant metabolites. This may be used, for example, to improve the stress tolerance of the plants or to improve the efficiency of transformation with foreign nucleic acid constructs.

Claim 1 and dependent claims involve a medium comprising a plant or part thereof. Thus, the amended claims are novel over the prior art disclosures. Although Yu(a) and Yu(b) may relate to the expression of α -1,4-glucan lyase in a host organism, such that it is capable of producing 1,5-D-anhydrofructose (AF), there is no mention of that organism being a plant. Rather, Yu(a) and (b) refer specifically to microorganisms such as bacteria, yeast and fungi. Indeed, Yu (a) and (b) are essentially concerned with the expression of α -1,4-glucan lyase and its subsequent use in the large-scale production of AF.

The skilled person concerned with obtaining α -1,4-glucan lyase in large quantities, for use in the large-scale production of AF and compounds such as the antibiotic microthecin, would not use plants for such a purpose; and, the transformation of microorganisms fails to teach or suggest transformation of plants or parts thereof. Further, Yu(a) and (b) are not concerned with improving the properties of plants or plant materials by *in situ* expression of α -1,4-glucan lyase. Thus, there is no incentive, teaching, or suggestion in Yu(a) and (b) to express α -1,4-glucan lyase in plants or parts thereof to produce antioxidants *in situ* from a glucan substrate.

Further, it is asserted by the Office Action that Poulsen, Ishida *et al.* and Perl *et al.* merely teach the transformation of potatoes, maize and grapes, respectively. While the transformation of plants was within the art, the Office Action has not shown a document which motivates the skilled person to even attempt to express an enzyme, for example α -1,4-glucan lyase, in a plant to produce *in situ* an anti-oxidant, for example AF, from a glucan substrate. & widely known in the art

The state of the law in the Federal Circuit requires that the suggestion or motivation to practice the claimed invention must be present in the cited art, and not gleaned from the Applicant's specification. Further, picking and choosing portions from a plethora of disparate

references in a hindsight attempt to formulate an obviousness rejection is prohibited. In the instant case, the only suggestion or motivation to provide for the recombinant expression of glucan-metabolizing enzymes in plants to produce anti-oxidants *in situ* is found in the Applicant's disclosure. Thus, the cited documents fail to teach or suggest the instant invention. A *prima facie* case of obviousness has not been made and the rejections of the claims have been obviated.

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In addition, the arguments in the Office Action with regard to obviousness, particularly with regard to the ease of plant transformation, apparently run counter to the Section 112 rejection; and, it is further respectfully asserted that the Examiner cannot have it both ways.

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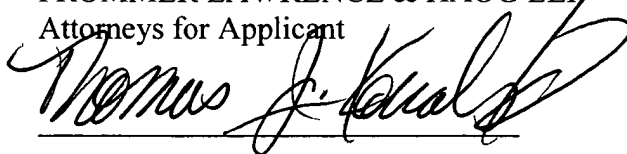
It is submitted therefore that none of the cited documents, either alone or in combination, would lead the skilled person to express, in a plant, a recombinant enzyme that acts on a glucan substrate to produce an anti-oxidant. Thus, Claims 1-18 are novel and inventive (non-obvious) over the cited art. Accordingly, reconsideration and withdrawal of the Section 103 rejection is believed to be in order and such action is respectfully requested.

CONCLUSION

In view of the remarks and amendments herewith, the application is believed to be in condition for allowance. Favorable reconsideration of the application and prompt issuance of a Notice of Allowance are earnestly solicited. The undersigned looks forward to hearing favorably from the Examiner at an early date.

Respectfully submitted,

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IN THE CLAIMS

1. A process for producing an anti-oxidant in a medium [comprising a component] which medium comprises[is] a plant or part thereof, and which process[method] comprises expressing in the plant[component] or part thereof a recombinant enzyme which acts on a glucan substrate present in the medium and/or the component or part thereof, to yield said anti-oxidant.
2. The[A] process according to claim 1, wherein the glucan comprises α -1,4 links.
3. The[A] process according to claim 2, wherein the glucan is starch.
4. The[A] process according to claim 1, wherein the enzyme is a glucan lyase.
5. The[A] process according to claim 4, wherein the enzyme is an α -1,4-glucan lyase.
6. The[A] process according to claim 5, wherein the enzyme is any one of the sequences shown as SEQ ID NOs[Nos] 1-6, or a variant, homologue or fragment thereof.
7. The[A] process according to claim 6, wherein the enzyme is any one of the sequences shown as SEQ ID NOs[Nos] 1-6.
8. The[A] process according to claim 4, wherein the enzyme is encoded by a nucleotide sequence comprising any one of the sequences shown as SEQ ID NOs[Nos] 7-12, or a variant, homolog[ue] or fragment thereof.
9. The[A] process according to claim 8, wherein the enzyme is encoded by a nucleotide sequence having any one of the sequences shown as SEQ ID NOs[Nos] 7-12.
10. The[A] process according to claim 1, wherein the anti-oxidant is produced in the plant component, or part thereof, and is then released into the medium.
11. The[A] process according to claim 1, wherein the anti-oxidant is anhydrofructose.

12. The[A] process according to claim 11, wherein the anti-oxidant is 1,5-D-anhydrofructose.
13. The[A] process according to claim 1, wherein the medium, is, or is used in the preparation of, a foodstuff.
14. The[A] process according to claim 13, wherein the foodstuff is a beverage.
15. The[A] process according to claim 14, wherein the beverage is an alcoholic beverage.
16. The[A] process according to claim 14, wherein the beverage is a wine.
17. The[A] process according to claim 1[13], wherein the plant[component] is all or part of a grape.
18. The[A] process according to claim 17, wherein the plant[component] is all or part of a grape.
19. [Use of anhydrofructose as] Method of imparting into a medium an anti-oxidant comprising the steps of adding into the medium[for a medium comprising] at least one component which is a plant or part thereof, wherein the anti-oxidant is anhydrofructose, and wherein the anhydrofructose is prepared *in situ* in the medium.
20. [Use of anhydrofructose as a means for] Method of imparting or improving stress tolerance in a plant, comprising administering anhydrofructose, wherein the anhydrofructose is prepared *in situ* in the plant.
21. [Use of anhydrofructose as a means for] Method of imparting or improving the transformation of a grape, comprising administering anhydrofructose, wherein the anhydrofructose is prepared *in situ* in the grape.
22. [Use of glucan lyase as a means for] Method of imparting or ^{stability}improving stress tolerance" in a plant, comprising administering glucan lyase, wherein the glucan lyase is prepared *in situ* in the plant.

23. [Use of glucan lyase as a means for]Method of imparting or improving the transformation of a grape, comprising administering glucan lyase, wherein the glucan lyase is prepared *in situ* in the grape.

24. [Use of a nucleotide sequence coding for a glucan lyase as a means for]Method of imparting or improving stress tolerance in a plant, comprising administering a nucleotide sequence coding for a glucan lyase, wherein the nucleotide sequence is expressed *in situ* in the plant.

25. [Use of a nucleotide sequence coding for a glucan lyase as a means for]Method of imparting or improving the transformation of a grape, comprising administering a nucleotide sequence coding for a glucan lyase, wherein the nucleotide sequence is expressed *in situ* in the grape.

**Comparison of glucan lyase aminoacid sequences of Sequence ID No. 1 against No.2-6****Part 1. Summary of the homologies of Sequence ID No. 1 against No.2-6**

Seq. ID. No.	1	2	3	4	5	6
Homology (%)	100	77.1	26.8	26.8	74.6	77.9

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Part 2. Pairwise comparisons of Seq No. 1 against No. 2-6**1. Sequence Id No. 1 (SIN1) aligned with Sequence Id No. 2 (SIN2)**

Sequence 1: SIN1, (1088 residues)
Sequence 2: SIN2, (1091 residues)

using the parameters:
Comparison matrix: BLOSUM62
Number of alignments computed: 20
Gap open penalty: 12
Gap extension penalty: 4

77.1% identity in 1096 residues overlap; Score: 4534.0; Gap frequency: 1.2%

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SIN1,      1 MFSTLAFVAPSALGASTFVGAEV-RSNVRIHSAFFAVHTATRKTNRNLNVSMTALSDKQTA
SIN2,      1 MYPTLTFVAPSALGARTFTCVGIFRSHILHSVPAVRLAVRKSNNRLNVSMSALFDKPTA
          * * * * *
SIN1,     60 TAGSTDNPDGIDYKTYDYVGWGFSPLSNTNWFAAGSSTPGGITDWTATMNVNFDRIDNP
SIN2,     61 VTGGKDNPDNINITYTIDYVVPWRFDPLSNTNWFAAGSSTPGDIDDWTATMNVNFDRIDNP
          * * * * *
SIN1,    120 SITVQHPVQVQVTSYNNNSYRVRFNPDGPIRDVTRGPILKQQLDWIRTQELSEGCDPGMT
SIN2,    121 SFTLEKPVQVQVTSYKNNCFRVRFNPDGPIRDVDRGPILQQLNWRKQEQSKGFDPKMG
          * * * * *
SIN1,    180 FTSEGFLTFETKDLNVIIYGNFKTRVTRKSDGKVMENDEVGTASSGNKCRGLMFVDRLY
SIN2,    181 FTKEGFLKFETKDLNVIIYGNFKTRVTRKRDGKIMENNEVPAGSLGNKCRGLMFVDRLY
          * * * * *
SIN1,    240 GNAIASVNKNFRNDAVKQEGFYGAGEVNCKYQDT-----YILERTGIAMTNYNDNLNY
SIN2,    241 GTAIASVNNENYRNDPDRKEGFYGAGEVNCFWDSEQNRNKYILERTGIAMTNYNDNINY
          * * * * *
SIN1,    294 NQWDLRPPHHDGALNPDIYIIPMYAAPWLIVNGCAGTS-EQYSYGWFMNDVNSQSYMNTGD
SIN2,    301 NQSDLIAPGYPS--DPNFIYIPMYFAAPWVVVKGCSGNSDEQYSYGWFMNDVNSQTYMNTGG
          * * * * *
SIN1,    353 TTWNSQGEDLAYMGAQYGPFDQHFFVYGAGGGMECVVTAFLSLQKKEFENQVLNKRSMVPP
SIN2,    359 TSWNCGEENLAYMGAQCGPFDQHFFVYGDGLEDVVAFLSLQKKEFENQVLNKRKRAVMPP
          * * * * *
SIN1,    413 KYVFGFFQGVFGTSSLLRAHMPAGENNISVEEIVEGYQNNNFPFEGLAVDVDMQDNLRVF
SIN2,    419 KYVFGYFQGVFGIASLLREQRPEGGNNISVQEIVEGYQSNFPFEGLAVDVDMQDNLRVF
          * * * * *
SIN1,    473 TTKGEFTWANKRVGTGGDPNNRSVFWEAHDKGLVCQTNITCFLRNDNEGQDYEVNQTLRER
SIN2,    479 TTKIEFTWANKVGTGGDSNNKSVFEAHDKGLVCQTNVTCFLRNDNGGADYEVNQTLREK
          * * * * *
SIN1,    533 QLYTKNDSLTTGTDFGMTDDGPSDAYIGHLDYGGGVECDALFPDWGRPDVAEWWGNKYKKL
SIN2,    539 GLYTKNDSLTTNFTGTNDGPSDAYIGHLDYGGGGNCDALFPDWGRPGVAEWWGDNYSKL
          * * * * *
SIN1,    593 FSIGLDFVWQDMTVPAMMPHKIGDDINVKPDGNWPNADDPNGQYNWKTYHPQVLVTDNR
SIN2,    599 FKIGLDFVWQDMTVPAMMPHKVGDVDRSPYGWPNEDEPSNGRYNWKSYHPQVLVTDNR
          * * * * *
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SIN1,      653 YENHGREPMVTQRNIHAYTLCESTRKEGIVENADTLTKFRRSYIISRGGYIGNQHFGGMW
SIN2,      659 YENHGREPMFTQRNMHAYTLCESTRKEGIVANADTLTKFRRSYIISRGGYIGNQHFGGMW
          *****

SIN1,      713 VGDNSTTSNYIQMMIANINNMNSCLPLVGS DIGGFTSYDNENQRT PCTGDLMVRYVQAG
SIN2,      719 VGDNSSSQRYLQMMIANIVNMNSCLPLVGS DIGGFTSYDGRNV---CPGDLMVRFVQAG
          *****

SIN1,      773 CLLPWFRNHYDRWIESKDHGKDYQELYMYPNEMDTLRKFVEFRYRWQEVLYTAMYQNAAF
SIN2,      776 CLLPWFRNHYGRLVEGKQEGKYYQELYMYKDEMATLRKFIEFRYRWQEVLYTAMYQNAAF
          *****

SIN1,      833 GKPIIKAASMYNDSNVRRQNDHFLLGHDGYRILCAPVVWENSTERELYLPVLTQWYK
SIN2,      836 GKPIIKAASMYDNDNRNVRGAQDDHFLLGHDGYRILCAPVVWENTTSRDLYLPVLTWKYK
          *****

SIN1,      893 FGPDEFDTKPLEGAMNGGDRIYNYPVPOSESPIFVREGAILPTRYTLNGENKSLNTYTDED
SIN2,      896 FGPDYDTKRLLDSALDGGQMIKNYSVPQSDSPIFVREGAILPTRYTL DGSNKSMTNTYTDD
          *****

SIN1,      953 PLVFEVFPPLGNNRADGMCYLLDDGGVTTNAEDNGKFSVVKVAAEQDGGTETITFTNDCEY
SIN2,      956 PLVFEVFPPLGNNRADGMCYLLDDGGITDAEDHGKFSVINVEALRKGVTTIKFAYDTYQY
          *****

SIN1,      1013 VFGGPFYVRVRGAQSPSNIHVSSGAGSQDMKVSSATSRAALFNDGENGDFWVDQETDSLW
SIN2,      1016 VFDGPFYVRIRNLTTASKINVSSGAGEEDMTPTSANSRAALFSDGGVGEYWADNDTSSLW
          *****

SIN1,      1073 LKLPNVVLPDAVITIT
SIN2,      1076 MKLPNLVLQDAVITIT
          *****

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2. Sequence Id No. 1 (SIN1) aligned with Sequence Id No. 3 (SIN3)

Identity : 286 (26.83%)

Similarity: 166 (15.57%)

Number of gaps inserted in GL1FULL: 59

Number of gaps inserted in MCSY1: 67

GL1FULL (=SIN1). Total number of residues: 1088.

MCSY1. (=SIN3). Total number of residues: 1066.

Comparison matrix : Structure-genetic matrix.

Open gap cost : 2

Unit gap cost : 2

The character to show that two aligned residues are identical is '|'

The character to show that two aligned residues are similar is '.'

Amino acids said to be 'similar' are: A,S,T; D,E; N,Q; R,K; I,L,M,V; F,Y,W

GL1FULL - M--FS-TLAFVAPSALGASTFVGAEVRSNVRIHSAFFPAVHTATRKTNRLN -47

| || | . | . . | | | .

MCSY1 - MAGFSDPLNFCKAEDYYS--VALDWKGPQKI--I-CVDTPPKSTKFP -43

GL1FULL - VSMTALSDKQTATAGSTDNPDGIDY-KTYDYGVWG--FSP-LSNTNWFA -93

| | | | |

MCSY1 - KNWHGVNLRF---DDGT--LGVVQFIRPC----VWRVRYDPGFKTSDEYG -84

GL1FULL - AGSSTPGGITDWTATMNVNFRIDN-PSITVQHPVQVQVTSYNNNS-YRV -141

. | . | . | . |

MCSY1 - DENTRTI-VQDYMSTLS---NKLDYRGLTWE-----TKCEDSGDF-F -122

GL1FULL - RFNPDGPIRDVTRGPILKQQL-DWIRTQELSEGCDPGMTFTSEGFLTFT -190

| . | . . | | | |

MCSY1 - TFS--SKVTAVEKSERTRNKVGDGLRIH-LWKS----P-FRIQVVRTLT -164

GL1FULL - -KDSLVIYGNFKTRVTRKSDCKVIMENDEVTASSGNKCRGLMFVDRLY -239

MCSY1 || | | . . || || | | |
 - LKDPYPI--PNVAAAEARVSD-KV-----VWQTSP--K-----TF--R-- -195
 GL1FULL - GNAIASVNKNFRN---DAVK--QEGFYGAGEVNCKYQDYLERTGIAMT -284
 MCSY1 - -KNLHPQHKMLKDTVLDIVKPGHGEYVGWGEEMGG-IQ--FMKEPT-F-MN -239
 GL1FULL - NYNYDNLNYNQWDLRPPHHDGALNP-DYYIPMYAAPWLI-VNGCAGTSE -332
 MCSY1 - YFNFDNMQYQQ--VYA---QGALDSRE---PLYHSDPFYLDVNS---NPE -278
 GL1FULL - QYSYCWFMNVSQSVMNT-GDTTWN SGQEDLAY--MGAQYGPFDQHFVYG -379
 MCSY1 - H-----KNITATFIDNYSQIAIDFGKTN SGYIKLGTRYGGID-CYGIS -320
 GL1FULL - AGGGMECVWTA FSLLQGEFENQVLNKR SVMPPKYVFGFFQGVFGTSSLL -429
 MCSY1 - ADTPE-IVRLYGLVGR---SKL--K-----PRYLGAHQACYGYQQ-- -357
 GL1FULL - RAHMPAGENNI-SVEIVEGYQNNNFPFEGLA VDVMQDNL RVFTTKGEF -478
 MCSY1 - -----ESDLYSV---VQYRDCKFPLDGIHVDVDVQDGFRTFTN--- -394
 GL1FULL - WTANRVGTGGDPNNRSVFE-WAHDKGLVCQTNITCFLRNDN-EGQDY--- -523
 MCSY1 - ---PHTF-----PNPKEMFTNL-RNNGIKCSTNITPVISINNREG-CYSTL -435
 GL1FULL - -E-VNQT--LRERQLYTKNDSL TGTD-----FG-----MTD-DGPSD -555
 MCSY1 - LEGVDKKYFIMD-DRYTEGTS GNAKDVRMYGGGNKVEVPNDVN GRPD -484
 GL1FULL - -----AYIGHLD---YG--CGV-----ECDALFPDWGRPDVAEWWGN NY -589
 MCSY1 - FKNYDFPANFNSKQYPYHGGVSYGYGNGSAGFY PDLNRKEVRIWWGMQY -534
 GL1FULL - KKLFSIGLDFVWQDMTPAMMPHK-IGDDINVKPDGNWPN---ADDPSNG -635
 MCSY1 - KYLFDMGLEFVWQDMT--TPAIHTSYGD-----MKG-LPTRLLV--TSDS -574
 GL1FULL - QYNWKTYHPQVLVTD MRYENHGREPMVTQRNIHAYTLCESTRKEGI--VE -683
 MCSY1 - -----VTNA---S-EKKLAIETWALYSYNLHKATWH-GLSRLE -607
 GL1FULL - NADLT LTKFRSYYISRGYIGNQHFGGMWVGDNSTTSNYIQMMIANNIM -733
 MCSY1 - S-----RKNKRNFILGRGSYAGAYRFAGLWTGDNASNWEFWKISVSQVLSL -653
 GL1FULL - NMSC LPLVGS DIGGFTSYDNEN--QRT PCTGDL MVRYVQAGCLLPWFRNH -781
 MCSY1 - GLNGVCIAGSDTGGFEPYRDANGVEEKYCSP ELLIRWYTG SFLLPWLRNH -703
 GL1FULL - YDRWIESKD HGKDYQELMYPN--E--MD-----TL-----RK FVEF -814
 MCSY1 - YVK-----KDR-KWFQEPYSYPKHLETHPELADQAWLYKSVLEICRY YVEL -748
 GL1FULL - RYRWQEVLYTAMYQNAAF GKPIIKAASMYNN-DSNVRR AQNDHFL----L -859
 MCSY1 - RYSLIQLLYDCMFQNVWDGMPITRSM LLTOTEDITFF-NESQKFLDNQYM -797

GL1FULL - YRVRFNPDGPIRDVTRGPILKQQLDWIRTQELSEGCDPGMTFTSEGFL-- -186
 | | . | | . | | . | |
 MVSU1 - Y-YTFKSEVTAVDET-----E--RTR--NKVGD-GLKI----YLWK -151

GL1FULL - -TFETKDLSEIYGNFKTRVTRKSDGKVMENDEVGTASSGNKCRGLMFV -235
 | . . . | . | | | | . |
 MVSU1 - NPFRIQWRLL-----TPLV---DPFPIP-N--VANATA----R---VA -182

GL1FULL - DRLYGNAIA-SVNKNFR--NDAVKQEGF--YGAGEVNCXYQDTYIL--ER -278
 | . . . | | . | | | | |
 MVSU1 - DKVWQTSPTKTRKNLHPQHMLKDTVLDIKPG-----HGEYVCWGEM -226

GL1FULL - TGIA-----MT--NY-NYDNLNYNQWDLRPPHHDGALNP-DYIIPMYAAP -320
 || | | | | | | | | | |
 MVSU1 - GGIEFMKEPTFMNYFNFDNMQYQQ--VYA---QGALDSRE---PLYHSDP -268

GL1FULL - WLI-VNGCACTSEQYSYGFMDNVSQSYMNT-GDTTWNSGQEDLAY--MG -366
 . | | | | | | | | | |
 MVSU1 - FYLDVNS---NPEH-----KNITATFIDNYSQIAIDFGKTNSGYIKLG -308

GL1FULL - AQYGPFDQHFVYGAGGMECVTAFSLLQGKEFENQVLNKRSMPPKYVF -416
 . | | | | | | | | | |
 MVSU1 - TRYGGID-CYGISADTVPE-IVRLYTGLVGR--SKL--K-----PRYL -346

GL1FULL - GFFQGVFGTSSLLRAHMPAGENNISVEIEGYQNNNFPFEGLAVDVDMQ -466
 | | | | | | | | | |
 MVSU1 - GAHQACYGYQQ-----ESDLHA--WQQYRDTKFPLDGLHVDVDFQ -385

GL1FULL - DNLRVFTTKG-EFWTANRVGTGGDPNNRSVF EWAHDKGLVCQTNITCFL- -514
 || || | | | | | | | |
 MVSU1 - DNFRFTTNPTF--PNPK-----EMFT-NL-----RNGIKCSTNITPVIS -424

GL1FULL - -RN--D-----NEGQD--Y-----EVN-----QTLR-----ERQL-Y -535
 | | | | | | | | | |
 MVSU1 - IRDRPNGYSTLNEGDKKYFIMDDRYTEGSGDPQNVRSFYGGGNPVEV -474

GL1FULL - TKNDSLTGDFG-----MTD-----DGPSDAYIGHLDYGGVECDALFPDW -576
 || . || | | | | | | | |
 MVSU1 - NPNDVWARPDFGDNYDFPTNFCKDYPYHGGVSY-GYNGTP--GYYPDL -521

GL1FULL - GRPDVAEWGNNYKLFISIGLDFVWQDMTPAMMPHKIGDDINVKPDGNW -626
 | | | | | | | | | |
 MVSU1 - NREEVRIWWGLQYEYLFNMGLEFVWQDMTPA-----IH-----SSY -558

GL1FULL - PNADDPSPNGQYNWKTYHPQVLVDMRYENHG-REPMVTQRNIHAYTLCES -675
 | | | | | | | | | |
 MVSU1 - ---GDM-KG-----LPTRLVTADSVTNASEKKLAIESWALYSYNLHKA -598

GL1FULL - TRKE-GIVENADTLTKFRSYIISRGYIGNQHFGGMWVDNSTTSNYIQ -724
 | | | | | | | | | |
 MVSU1 - TFHGLGRLES----RKNKRNFILGRGSYAGAYRFAGLWTDGNASTWEFWK -644

GL1FULL - MMIANNINMMSCLPLVGSDIGGFTSYDNE-NQRTPTCTGDLMVRYVQAGC -773
 || || | | | |
 MVSU1 - ISVSQVLSLGLNGVCIAGSDTGGFEPARTEIGEKEYCPELLIRWYTGsf -694

GL1FULL - LLPWFRNHYDRWIESKDHGKDYQELYMYPNEMDT---L-----R----- -809
 ||| ||| . || | | | | | |

[illegible]

Comparison of glucan lyase aminoacid sequences of Sequence ID No. 1 against No.2-6

Part 1. Summary of the homologies of Sequence ID No. 1 against No.2-6

Seq. ID. No.	1	2	3	4	5	6
Homology (%)	100	77.1	26.8	26.8	74.6	77.9

Part 2. Pairwise comparisons of Seq No. 1 against No. 2-6

1. Sequence Id No. 1 (SIN1) aligned with Sequence Id No. 2 (SIN2)

Sequence 1: SIN1, (1088 residues)
Sequence 2: SIN2, (1091 residues)

using the parameters:
Comparison matrix: BLOSUM62
Number of alignments computed: 20
Gap open penalty: 12
Gap extension penalty: 4

77.1% identity in 1096 residues overlap; Score: 4534.0; Gap frequency: 1.2%

```
SIN1,      1 MFSTLAFVAPSALGASTFVGAEV-RSNVRIHSAFFAVHTATRKTNRLNVSMTALSDKQTA
SIN2,      1 MYPTLTFVAPSALGARTFTCVGIFRSHILHSVVPVAVRLAVRKSNNRLNVSMSALFDKPTA
          * ** ***** **          *** ** * ** ***** ** * **

SIN1,     60 TAGSTDNPDGIDYKTYDYVGWGFSPLSNTNWFAAGSSTPGGITDWTATMNVNFDRIDNP
SIN2,     61 VTGKDNPDNINITYTIDYVPVWRFDPLSNTNWFAAGSSTPGDIDDWTATMNVNFDRIDNP
          * **** * * ***** * * ***** ***** * ***** *****

SIN1,    120 SITVQHPVQVQVTSYNNNSYRVRFNPDGPIRDVTRGPILKQQLDWIRTQELSEGCDPGMT
SIN2,    121 SFTLEKPVQVQVTSYKNNCFRVRFNPDGPIRDVDRGPILQQLNWRKQEQSKGFDPKMG
          * ** ***** ** ***** ***** ***** ** * ** *

SIN1,    180 FTSEGFLTFFETKDLVVIYGNFKTRVTRKSDGKIVIMENDEVGTASSGNKCRGLMFVDRLY
SIN2,    181 FTKEGFLKFETKDLNVIYGNFKTRVTRKRDGKGIMENNEVPAGSLGNKCRGLMFVDRLY
          ** ***** ***** ***** ***** ** * *****

SIN1,    240 GNAIASVNKNFRNDAVKQEGFYGAGEVNCKYQDT-----YILERTGIAMTNYNYNLNY
SIN2,    241 GTAIASVNNENYRNDPDRKEGFYGAGEVNCEFDWSEQNRNKYILERTGIAMTNYNYNLNY
          * ***** * ** ***** * ***** *****

SIN1,    294 NQWDLRPPHHDGALNPDIYIPMYAAPWLIVNGCAGTS-EQYSYGWFMNDVNSQSYMNTGD
SIN2,    301 NQSDLIAPGYPS--DPNFIYIPMYFAAPWVVVKGCSGNSDEQYSYGWFMNDVNSQTYMNTGG
          ** * * * ***** * ***** ***** * ** * *****

SIN1,    353 TTWNSGQEDLAYMGAQYGPFDQHFVYGAGGGMECVVTAFSLLQGKEFENQVLNKRSMVMP
SIN2,    359 TSWNCGEENLAYMGAQCGPFDQHFVYGDGDGLEDVVQAFSLLQGKEFENQVLNKRSMVMP
          * ** * * ***** ***** * ** * *****

SIN1,    413 KYVFGFFQGVFGTSSLLRAHMPAGENNISVEEIVEGYQNNNFPFEGLAVDVDMQDNLRVF
SIN2,    419 KYVFGYFQGVFGIASLLREQRPEGNNISVQEIVEGYQSNNFPLEGLAVDVMQDNLRVF
          ***** ***** ** * ***** ***** ***** *****

SIN1,    473 TTKGEFTANRVGTGGDPNNRSVFWEAHDKGLVCQTNITCFLRNDNEGQDYEVNQTLRER
SIN2,    479 TTKIEFTANKVGTGGDSNNKSVFEAHDKGLVCQTNVTCFLRNDNGGADYEVNQTLREK
          *** ***** ***** ***** ***** ***** ***** *****

SIN1,    533 QLYTKNDSLTTGTDFGMTDDGPSDAYIGHLDYGGGVECDALFPDWGRPDVAEWWGNKYKL
SIN2,    539 GLYTKNDSLTTNFGTTNDGPSDAYIGHLDYGGGGNCDALFPDWGRPGVAEWWGDNYSKL
          ***** * ** * ***** ***** ***** *****

SIN1,    593 FSIGLDFVWQDMTVPAMMPHKIGDDINVKPDGNWPNADDPNGQYNWKTYHPQVLVTDNR
SIN2,    599 FKIGLDFVWQDMTVPAMMPHKVGDAVDTRSPYGWPNENDPSNGRYNWKSYHPQVLVTDNR
          * ***** ***** **          *** ***** ***** *****
```

```

SIN1,      653 YENHGREPMVTQRNIHAYTLCESTRKEGIVENADTLTKFRRSYIISRGGYIGNQHFGGMW
SIN2,      659 YENHGREPMFTQRNMHAYTLCESTRKEGIVANADTLTKFRRSYIISRGGYIGNQHFGGMW
          *****

SIN1,      713 VGDNSTTSNYIQMMIANINNMNSCLPLVGS DIGGFTSYDNENQRT PCTGDLMVRYVQAG
SIN2,      719 VGDNSSSQRYLQMMIANIVNMNSCLPLVGS DIGGFTSYDGRNV--CPGDLMVREVQAG
          *****

SIN1,      773 CLLPWFRNHYDRWIESKDHGKDYQELMYPNEMDTLRKFVEFRYRWQEVLYTAMYQNAAF
SIN2,      776 CLLPWFRNHYGRLVEGKQEGKYYQELMYKDEMATLRKFIEFRYRWQEVLYTAMYQNAAF
          *****

SIN1,      833 GKPIIKAASMYNDSNVRRQAQNDHFLLGHDGYRILCAPVVWENSTERELYLPVLTQWYK
SIN2,      836 GKPIIKAASMYDNDRNVRGQDDHFLLGHDGYRILCAPVVWENTTSRDLYLPVLTQWYK
          *****

SIN1,      893 FGPPDFDKPLEGAMNGGDRIYNYPVPSQSESPFVREGAILPTRYTLNGENKSLNTYTDED
SIN2,      896 FGPDYDTKRLDSDGCGQMIKNSVPQSDSPIFVREGAILPTRYTLGDSNKSMTYTDDK
          *****

SIN1,      953 PLVFEVFPLGNNRADGMCYLDGGVTTNAEDNGKFSVVKVAAEQDGGTETITFTNDCEY
SIN2,      956 PLVFEVFPLGNNRADGMCYLDGGITDAEDHGKFSVINVEALRKGVTTIKFAYDTYQY
          *****

SIN1,     1013 VFGGPFYVRVRGAQSPSNIHVSSGAGSQDMKVSSATSRAALFNDGENGDFWVDQETDSLW
SIN2,     1016 VFDGPFYVRIRNLTTASKINVSSGAGEEDMTPTSANSRAALFSDGGVGEYWDNDTSSLW
          *****

SIN1,     1073 LKLPNVVLPDAVITIT
SIN2,     1076 MKLPNLVLQDAVITIT
          *****

```

2. Sequence Id No. 1 (SIN1) aligned with Sequence Id No. 3 (SIN3)

Identity : 286 (26.83%)

Similarity: 166 (15.57%)

Number of gaps inserted in GL1FULL: 59

Number of gaps inserted in MCSY1: 67

GL1FULL (=SIN1). Total number of residues: 1088.

MCSY1. (=SIN3). Total number of residues: 1066.

Comparison matrix : Structure-genetic matrix.

Open gap cost : 2

Unit gap cost : 2

The character to show that two aligned residues are identical is '|'

The character to show that two aligned residues are similar is '.'

Amino acids said to be 'similar' are: A,S,T; D,E; N,Q; R,K; I,L,M,V; F,Y,W

```

GL1FULL  - M--FS-TLAFVAPSALGASTFVGAEVRSNVRIHSAFPAVHTATRKTNRLN -47
          | || | | . | . . | | | | .
MCSY1    - MAGFSDDLNFCKAEDYYS--VALDWKGPQKI--I-GVDTPPKSTKFP -43

GL1FULL  - VSMTALSDKQTATAGSTDNDPGIDY-KTYDYVCVWG--FSP-LSNTNWFA -93
          | . . . | | | | . . .
MCSY1    - KNWHGVNLRF---DDGT--LGWQFIRPC----VWRVRYDPGFKTSDEYG -84

GL1FULL  - AGSSTPGGIDTWTATMNVNFRIDN-PSITVQHPVQVQVTSYNNNS-YRV -141
          . . | . | . | | | | .
MCSY1    - DENTRTI-VQDYMSTLS---NKLDTYRGLTWE-----TKCEDSGDF-F -122

GL1FULL  - RFNPDGPIRDVTRGPILKQQL-DWIRTQELSEGCDPGMTFTSEGFLTFT -190
          | . . | . . | | | | |
MCSY1    - TFS--SKVTAVEKSERTRNKVCDGLRIH-LWKS----P-FRIQWRTLTP -164

GL1FULL  - -KDSLVIYGNFKTRVTRKSDGKVMENDEVGTASSGNKCRGLMFVDRLY -239

```

MCSY1 || | | . || || | | | |
 - LKDPYPI--PNVAAAEARVSD-KV-----VWQTSP--K----TF--R-- -195

 GL1FULL - GNAIASVNKNFRN---DAVK--QEGFYGAGEVNCKYQDTYILERTGIAMT -284
 MCSY1 - -KNLHPQHKMLKDTVLDIVKPGHGEYVGWGEEMGG-IQ--FMKEPT-F-MN -239

 GL1FULL - NYNYDNLNYNQWDLRPPHHDGALNP--DYYIPMYAAPWLI-VNGCAGTSE -332
 MCSY1 - YFNFDNMQYQQ--VYA---QGALDSRE---PLYHSDPFYLDVNS---NPE -278

 GL1FULL - QYSYGFWMNVQSVMNT-CDTTWNSGQEDLAY--MGAQYGPFDQHfVYG -379
 MCSY1 - H-----KNITATFIDNYSQIAIDFGKTNsgYIKLgTRYGGID-CYGIS -320

 GL1FULL - AGGMECVWTAfSLLQGKEFENQVLNKRsvMPPKYVgFFQGVfGTSSLL -429
 MCSY1 - ADTPE-IVRLYGLVGR---SKL--K-----PRYLGAHQACyGYQQ-- -357

 GL1FULL - RAHMPAGENNI-SVEEIVEGYQNNNFPEGLAVDvDMQDNLrvFTTKGEF -478
 MCSY1 - -----ESDLYSV---VQYRDCKfPLDGIHVDVDVQDGFRTFTTN--- -394

 GL1FULL - WTANRVGTGGDPNNRSVFE-WAHDKGLVCQTnitCFLRNDN-EGQDY--- -523
 MCSY1 - ---PHTF-----PNPKEMFTNL-RNNGIKCSTNITPVISINNREG-CYSTL -435

 GL1FULL - -E-VNQT--LRERQLYTKNDSLtGTD-----FG-----MTD-DGpSD -555
 MCSY1 - LEGVDKkyfIMD-DRYTEGTSGNAKDVRYMYGGGNKVEVDpNDVNGRPD -484

 GL1FULL - -----AYIGHLD---YG--GGV-----ECDALFPDWGRPDVAEWwGNNY -589
 MCSY1 - FKDNyDFANfNSKQYPYHGVSyGYNGSAGfYpDLNRKEVRIwwGMQY -534

 GL1FULL - KKLfSIGLDFVwQDMtVPAMMPHK-IGDDINVKPDGNWPN---ADDPsNG -635
 MCSY1 - KYLFDMGLEfVwQDMT--TPAIHTSYGD-----MKG-LPTRLLV--TSDS -574

 GL1FULL - QYNWKTYHPQVLVTDMRYENHGRePMVTQRNIHAYTLCESTRKEGI--VE -683
 MCSY1 - -----VTNA---S-EKKLAietWALYSYNLHKATWH-GLSRLE -607

 GL1FULL - NADTLTKFRRSYIISRGYIGNQHfGGMWwGDNSTTSNYIQMMIANNIM -733
 MCSY1 - S-----RKNKRNFILGRGSYACAYRfAGLWTGDNASNWEfWKISVSQVLSL -653

 GL1FULL - NMSCLPLVGSdIGGfTSYDNEN--QRTpCTGDLmVRYVQAGCLLPWFRNH -781
 MCSY1 - GLNGVCIAGSDTGGfEPYRDANGVEEKYCSPELLIRWYTCsFLLPWLrNH -703

 GL1FULL - YDRWIESKDHGKDYQELyMPN--E--MD-----TL----RKfVEF -814
 MCSY1 - YVK----KDR-KWfQEPYSYPKHLEThPELADQAWLYKSVLEICRYyVEL -748

 GL1FULL - RYRWQEVLYTAMyQNAAFGKPIIKAASMYNN-DSNVRRaQNDHFL----L -859
 MCSY1 - RYSLIQLLYDCMfQNVWDGMPITRSMLLTDtEDTfFF-NESQKFLDNQYM -797

```

GL1FULL  - GGHDCGYRILCAPVWENS-TE-----RELYLPVLTQWY--KFGP-DFDT- -899
          || || ||.. || | | |.. || | | |
MCSY1    - AGDD---ILVAPIL--HSRKEIPGENRDVYLPYHTWYPSNLRPWD-DQG -841

GL1FULL  - ----KPLEGAM--NGGDRIY---NYPVPQSESPIFVREGAILPTRYTLNG -940
          |.. | | | | | | | | | | | | |
MCSY1    - VALGNPVEGGSVINYTARIVAPEDYNLFHSWVPVYVREGAIIPQ---I--- -886

GL1FULL  - ENKSLNTYTDEDPLVFEVFPLGNNRADGMCYLDDGGVTTNA--EDNGKFS -988
          | . . . . . | | | | | | | | |
MCSY1    - EVRQWTGQGGANRIKFNIYP-GKDKEYCT-YLDDG-VSRDSAPED---LP -930

GL1FULL  - VKVAEQD--GGTETIT--F-TNDCEYVFG-GP----FYVRVGAQSP -1028
          | . || | | | | | | | | | | |
MCSY1    - QYKETHEQSKVEGAE-IAKQIGKKTGYN-ISGTDPEAKGYHRKVAVTQTS -978

GL1FULL  - SNIHVSSGAGSQDMKVSS-ATSRAA-----L-----FNDG----- -1057
          . . . . | | | | |
MCSY1    - KD---KTRTVTIEPKHNGYDPSKEVGDDYYTIILWYAPGFDGSIVDVSKTT -1025

GL1FULL  - ENGDFWVDQE----TD--SLWLKLPNVWL--PDAV-ITIT -1088
          | . | . | . . . | | | | |
MCSY1    - VNVEGGVEHQVYKNSDLHTVIDV-KEVIGTTKSVKITCTAA -1066

```

3. Sequence Id No. 1 (SIN1) aligned with Sequence Id No. 4 (SIN4)

Identity : 287 (26.82%)

Similarity: 160 (14.95%)

Number of gaps inserted in GL1FULL: 64

Number of gaps inserted in MVSU1: 63

* ALIGNMENT OF TWO PROTEIN SEQUENCES. *

The two sequences to be aligned are:

GL1FULL (=SIN1). Total number of residues: 1088.

MVSU1 (=SIN4). Total number of residues: 1070.

Comparison matrix : Structure-genetic matrix.

Open gap cost : 2

Unit gap cost : 2

The character to show that two aligned residues are identical is '|'

The character to show that two aligned residues are similar is '.'

Amino acids said to be 'similar' are: A,S,T; D,E; N,Q; R,K; I,L,M,V; F,Y,W

```

GL1FULL  - MFSTLAFVAPSALGAS-TFVGAEVRSNVRIHSAFPAVH--TATRKTNRLN -47
          | . . . | | | | | | | |
MVSU1    - M-----AGLSDDLNFCKAE---DY-----YAAAKGWSGPQKIIRYD -33

GL1FULL  - VSMTALSDKQTATAGSTDN-P--DGIDYKTYDYVG--VWG--FSP-LSNT -89
          . | . . | | | | | | | |
MVSU1    - QTP-PQGTKD-PKSWHAVNLPFDDGTMCVV-QFVRPCVWRVRYDPSVKTS -80

GL1FULL  - NWFAGSSTPGGITDWTATMNVNFDRIDNPSITVQHPVQVQVTSYNNNS- -138
          . . . . | . | | | | |
MVSU1    - DEYGDENTRTI-VQDYMTTLVGNLDIF--RGLTW-----VSTLEDSCGE -120

```

GL1FULL - YRVRFNPDGPIRDVTRGPILKQQLDWIRTQELSEGCDPGMTFTSEGFL-- -186
 | | . | | . | | . | |
 MVS1 - Y-YTFKSEVTAVDET-----E--RTR--NKVGD-GLKI----YLWK -151

 GL1FULL - -TFETKDLSVIYGNFKTRVTRKSDGKVMENDEVGTASSGNKCRGLMFV -235
 | . . . | . | | | | . |
 MVS1 - NPFRIQVRL-----TPLV---DPFPI-P-N--VANATA----R---VA -182

 GL1FULL - DRLYGNAIA-SVNKNFR--NDAVKQEGF--YGAGEVNCKYQDTYIL--ER -278
 | . . . | | . | | | | |
 MVS1 - DKVWWTSPKTFRKNLHPQHKMLKDTVLDIIPKPG-----HGEYVGWCEM -226

 GL1FULL - TGIA-----MT--NY-NYDNLNYNQWDLRPPPHDGLNP-DYIIPMYAAP -320
 || | || | | | | | | | |
 MVS1 - GGIEFMKEPTFMNYFNFDNMQYQQ--VYA---QCALDSRE---PLYHSDP -268

 GL1FULL - WLI-VNGCAGTSEQYSYGWFMNVQSQSYMNT-GDTTWNSGQEDLAY--MG -366
 . . || | | | | | | | |
 MVS1 - FYLDVNS---NPEH-----KNITATFIDNYSQIAIDFGKTNISGYIKLG -308

 GL1FULL - AQYGPFDQHFVYGAGGMECWTAFLSLQKQEFENQVLNKRSMPPKYVF -416
 . || | . | | | . | | | | |
 MVS1 - TRYGGID-CYGISADTVPE-IVRLYTGLVGR---SKL--K-----PRYL -346

 GL1FULL - GFFQGVFGTSSLLRAHMPAGENNISVEEIVEGYQNNNFPFEGLAVDVDMQ -466
 | | | | | | | | | | | | |
 MVS1 - GAHQACYGYQQ-----ESDLHA--VQYRDTKFPLDGLHVDVDFQ -385

 GL1FULL - DNLRVFTTKG-EFWTANRVGTGGDPNNRSVFEWAHDKGLVCQTNITCFL- -514
 || || | | | | | | | | |
 MVS1 - DNFRFTTNPIF--PNPK-----EMFT-NL-----RNNGIKSTNITPVIS -424

 GL1FULL - -RN--D-----NEGQD--Y-----EVN----QTLR-----ERQL-Y -535
 | | | | | | | | | |
 MVS1 - IRDRPNGYSTLNEGYDKKYFIMDDRYEGTSGDPQNVRYSFYGGGNPVEV -474

 GL1FULL - TKNDSLTGDFG-----MTD-----DGPSDAYIGHLDYGGGVECDALFPDW -576
 || . || | | | | | | | |
 MVS1 - NPNDVWARPDFGDNYDFPTNFCKDYPYHGGVSY-GYNGTP--GYPD -521

 GL1FULL - GRPDVAEWGNNYKLFSGLDVFWQDMTPAMPHKIGDDINVKPDGNW -626
 | | | | | | | | | | | |
 MVS1 - NREEVRIWWGLQYEYLFNMGLEFVWQDMTPA-----IH----SS -558

 GL1FULL - PNADDPNSGQYNWKYHPQVLVDMRYENHG-REPMVTQRNIHAYTLCES -675
 | | | | | | | | | | |
 MVS1 - ---GDM-KG-----LPTRLVTADSVTNASEKKLAIESWALYSYNLHKA -598

 GL1FULL - TRKE-GIVENADTLTKFRRSYISRGYIGNQHFGGMWVGDNSTTSNYIQ -724
 | | | | | | | | | | | |
 MVS1 - TFHGLGRLES-----RKNKRNFILGRGSYAGAYRFAGLWTGDNASTWEFWK -644

 GL1FULL - MMIANNINMNSCLPLVGSDIGGFTSYDNE-NQRTPTGDLMVRYVQAGC -773
 || | | | | | | |
 MVS1 - ISVSQVLSLGLNGVCIAGSDTGGFEPARTEIGEKEYCPELLIRWYTGSF -694

 GL1FULL - LLPWFRNHYDRWIESKDHGKDYQELYMYPNEMDT---L-----R----- -809
 ||| ||| . | | | | | | |

MVSY1 - LLPWLRNHYVK----KDR-KWFQEPYAYPKHLETHPELADQAWLYKSVLE -739

GL1FULL - --KF-VEFRYRWQEVLTYAMYQNAA----FGK-PIKAA--SMYNNSNV -849
 .. || || .. || |.. . . . |..

MVSY1 - ICRYWVELRSLIQLLYDCMFQNVVDGMP LARSMLLTDTEDTTFNESQ- -788

GL1FULL - RRAQNDHFLLGCHDGYRILCAPVWENS-TE-----RELYLPVLTQWY-- -891
 . . || || ||. | | |.. ||

MVSY1 - -KFLDNQYM-AGDD---ILVAPIL--HSRNEVPGENRDVYLPLFHTWYPS -831

GL1FULL - KFGP-DFDT-----KPLEGAM--NGGDRIY---NYPVPQSESPIFVREGA -930
 ||| |.. | || |. |..|||

MVSY1 - NLRPWD-DQGVALGNPVEGGSVINYTARIVAPEDYNLFHNWVPVYIREGA -880

GL1FULL - ILPT--RYTLNGENKSLNTYTDDEPLVFEVPLGNNRADGMCYLDDGGV -977
 |.. | || |.. |..| | |||| |

MVSY1 - IIPQIQVR-QWIGE--G-----GPNPIKFNYP-GKDKEYVT-YLDDG-V -919

GL1FULL - TTNAEDNGKFSWKVAAEQD--GGTET---ITF-----TNDCEYVFGGP -1017
 . . || ||. . ||| |

MVSY1 - SRDSAPDD-LPQYREAYEQAKVEGKDQKQLAVIQGNKTND-----FSAS -963

GL1FULL - FYVR-VRGAQSPSNI-HVS---SGAGSQDMKVSS-ATSRAA-----LF -1054
 . | | | . . . | |.

MVSY1 - GIDKEAKGYHRKVSQKESKDKTRTVTIEPKHNGYDPSKEVGNYTILW -1013

GL1FULL - NDGE-NGDFWVD--QETDSL--WLK-----LPNVLPDA--VI-T-- -1086
 | || | . | || ||

MVSY1 - YAPGFDGSI-VDVSQATVNIIEGGVECEIFKNTGLHTVWV-NVKEVIGTTK -1061

GL1FULL - ---IT -1088
 ||

MVSY1 - SVKITCTTA -1070

4. Sequence Id No. 1 (SIN1) aligned with Sequence Id No. 5 (SIN5)

Sequence 1: SIN1, (1088 residues)
 Sequence 2: SIN5, (1092 residues)

using the parameters:
 Comparison matrix: BLOSUM62
 Number of alignments computed: 20
 Gap open penalty: 12
 Gap extension penalty: 4

74.6% identity in 1096 residues overlap; Score: 4455.0; Gap frequency: 1.3%

SIN1, 1 MFSTLAFVAPSALGASTFVGAEVRSNVRIHSAFFAVHTATRKTNRNLNVSM TALSDKQTAT
 SIN5, 1 MFPTLTFFIAPSALAASTFVGADIRSGIRIQSALPAVRNAVRRSKHYNVSM TALSDKQTAT
 * * * * *

SIN1, 61 AGSTDNPDGIDYKTYDYVGWGFSPLSNTNWFAAGSSTPGGITDWTATMNVNFDRI DNPS
 SIN5, 61 SIGPDNPDGINYQNYDIIPVAGFTPLSNTNWYAAGSSTPGGITDWTATMNVKFDRI DNPS
 * * * * *

SIN1, 121 ITVQHPVQVQVTSYNNNSYRVRFNPDGPIRDVTRGPILKQQLDWIRTQELSEGCDPGMTF
 SIN5, 121 YSNHFPVQIQVTSYNNNSFRIRFNPDPGPIRDVSRGPILKQQLTWIRNQELAQCNCNPNMSF
 * * * * *

SIN1, 181 TSEGFLTFTKDL SVIIYGNFKTRVTRKSDGKVMIMENDEVTASSGNKCRGLMFVDRLYG
 SIN5, 181 SPEGFLSFETKDLNVIYGNCKMRVTKK-DGYLVMENDECNSQSDGNKCRGLMYVDRLYG
 * * * * *

SIN1, 241 NAIASVNKNFRNDAVKQEGFYGAGEVNCYQD-----TYILERTGIAMTNYNDNLNYNQ
 SIN5, 240 NAIASVQTNFHKDTSRNEKFYGAGEVNCRYEEQGKAPTYVLERSGLAMTNYNDNLNYNQ
 * * * * *


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SIN6,      118  GLNIRSAMPKPYVGFQFQGVFGATSLLRDNLPAENNVSLEEIVEGYQNQNVFPEGLAVD
          ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
SIN1,      463  VDMQDNLRVFTTKGEFTANRVGTGGDPNNRSVFEWAHDKGLVCQTNITCFLRNDNEGQD
SIN6,      178  VDMQDDLRVFTTRPAFWTANKVGGGDPNNKSVFEWAHDRGLVCQTNVTCFLK--NEKNP
          ***** * * * * * * * * * * * * * * * * * * * * * * * * * *
SIN1,      523  YEVNQTLRERQLYTKNSLTGTDFGMDTDDGSPDAYIGHLDYGGGVECDALFPDWGRPDVA
SIN6,      236  YEVNQSLREKQLYTKSDSLDNIDFGTTPDGSPDAYIGHLDYGGGVECDALFPDWGRPDVA
          ***** * * * * * * * * * * * * * * * * * * * * * * * * * *
SIN1,      583  EWWGNNYKKLFSIGLDFVWQDMTPVAMMPHKIGDDINVKPDGN--WPNADDPNSNGQYNW
SIN6,      296  QWWGDNKYKKLFSIGLDFVWQDMTPVAMMPHRLGDPVGTNSGETAPGWPNDKDPSNGRYNW
          *** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
SIN1,      640  KTYHPQVLVTDMMRYENHGREPMVTQRNIHAYTLCESTRKEGIVENADTLTKFRRSYIISR
SIN6,      356  KSYHPQVLVTDMMRYDDYGRDPIVTRNLHAYTLCESTRREGIVGNADSLTKFRRSYIISR
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
SIN1,      700  GGYIGNQHFGGMWVGDNSTTSNYIQMMIANNINNMMSCLPLVGSDIGGFSTYDNENQRTF
SIN6,      416  GGYIGNQHFGGMWVGDNSTEDYLAMMVINVINNMMSGVPLVGSDIGGFTEHDKRN---P
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
SIN1,      760  CTGDLMVRYVQAGCLLPWFRNHYDRWIESKDHGKDYQELYMYPNEMDTLRKFVEFRYRWQ
SIN6,      473  CTPDLMMRFVQAGCLLPWFRNHYDRWIESKKHGKNYQELMYRDLHDALRSFVELRYRWQ
          ** * * * * * * * * * * * * * * * * * * * * * * * * * * * *
SIN1,      820  EVLYTAMYQNAAFGKPIIKAASMYNNDSNVRRQNDHF
SIN6,      533  EVLYTAMYQNALNGKPIIKTVSMYNNDMNVKDAQNDHF
          ***** * * * * * * * * * * * * * * * * * * * * * * * *

```

===03-MAY-2001=====NALIGN=====PC/GENE===

* ALIGNMENT OF TWO NUCLEOTIDE SEQUENCES. *

The two sequences to be aligned are:

SEQIDN07.

Total number of bases: 3267.

SEQIDN08.

Total number of bases: 3276.

Open gap cost : 50

Unit gap cost : 20

The character to show that two aligned residues are identical is '|'

```
SEQIDN07 - ATGTTTTC AACCTT GCGTTT GTCGCACCTAGT GCGCTGGGAGCCAGTAC -50
          ||| | ||||| | | | | | | | | | | | | | | | | |
SEQIDN08 - ATGTATCCAACCTCACTTCGTGGCGCCTAGT GCGCTAGGGGCCAGAAC -50

SEQIDN07 - CTTCGTAGGGGCGGAGGTC---AGGTCAAATGTTGTTATCCATTCCGCTT -97
          || | | | | | | | | | | | | | | | | | | | |
SEQIDN08 - TTTCACGTGTGTGGGCATTTT TAGGTCACACATTCTTATTCATTTCGGTTG -100

SEQIDN07 - TTCCAGCTGTGCACACAGCTACTCGCAAACCAATCGCCTCAATGTATCC -147
          ||||| |||| | || | | | | | | | | | | | | | |
SEQIDN08 - TTCCAGCGGTGCGTCTAGCTGTGCGCAAAGCAACCGCCTCAATGTATCC -150

SEQIDN07 - ATGACCGCATTGTCCGACAAACAAACGGCTACTGCGGGTAGTACAGACAA -197
          || | |||| | | | | | | | | | | | | | | | | |
SEQIDN08 - ATGTCCGCTTTGTTGACAAACCGACTGCTGTTACTGGAGGGAAGGACAA -200

SEQIDN07 - TCCGGACGGTATCGACTACAAGACCTACGATTACGTCCGAGTATGGGGTT -247
          ||||| |||| | || | | | | | | | | | | | | | |
SEQIDN08 - CCCGGACAATATCAATTACACCACTTATGACTACGTCCCTGTGTGGCGCT -250

SEQIDN07 - TCAGCCCCCTCTCAACACGAACTGGTTTGCTGCCGGCTCTTCTACCCCG -297
          || | |||| | | | | | | | | | | | | | | | | |
SEQIDN08 - TCGACCCCTCAGCAATACGAACTGGTTTGCTGCCGGATCTTCACTCCC -300

SEQIDN07 - GGTGGCATCACTGATTGGACGGCTACAATGAATGTCAACTTCGACCGTAT -347
          || | || | | | | | | | | | | | | | | | | | |
SEQIDN08 - GGCGATATTGACGACTGGACGGCGACAATGAATGTGAACTTCGACCGTAT -350

SEQIDN07 - CGACAATCCGTCCATCACTGTCCAGCATCCCGTTCAGGTTTCAGGTCACGT -397
          ||||| || | || | | | | | | | | | | | | | | | |
SEQIDN08 - CGACAATCCATCCTTCACTCTCGAGAAACCGGTTTCAGGTTTCAGGTCACGT -400

SEQIDN07 - CATACAACAACAACAGCTACAGGGTTCGTTCAACCCTGATGGCCCTATT -447
          ||||| |||| | | | | | | | | | | | | | | | | |
SEQIDN08 - CATACAAGAACAATTGTTTCAGGGTTCGTTCAACCCTGATGGTCCTATT -450
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SEQIDN07 - CGTGATGTGACTCGTGGGCCTATCCTCAAGCAGCAACTAGATTGGATTCC -497
|| ||||| ||||||||||||||| ||||||||| ||||| ||
SEQIDN08 - CGCGATGTGGATCGTGGGCCTATCCTCCAGCAGCAACTAAATTGGATCCG -500

SEQIDN07 - AACGCAGGAGCTGTCAGAGGGATGTGATCCCGAATGACTTTCACATCAG -547
| ||||| ||| ||| | ||||| ||| ||||| ||
SEQIDN08 - GAAGCAGGAGCAGTCGAAGGGGTTGATCCTAAGATGGGCTTCACAAAAG -550

SEQIDN07 - AAGGTTTCTTGACTTTTGAGACCAAGGATCTAAGCGTCATCATCTACGGA -597
||||||| ||||||||||||| ||| ||||| |||
SEQIDN08 - AAGGTTTCTTGAAATTTGAGACCAAGGATCTGAACGTTATCATATATGGC -600

SEQIDN07 - AATTTCAAGACCAGAGTTACGAGAAAGTCTGACGGCAAGGTCATCATGGA -647
||||| ||||| ||||||||| ||| ||||| |||||
SEQIDN08 - AATTTTAAGACTAGAGTTACGAGGAAGAGGGATGGAAAAGGGATCATGGA -650

SEQIDN07 - AAATGATGAAGTTGGAATGCATCGTCCGGGAACAAGTGCCGGGGATTGA -697
||| ||||| | ||||| |||||||||||||||
SEQIDN08 - GAATAATGAAGTGCCGGCAGGATCGTTAGGGAACAAGTGCCGGGGATTGA -700

SEQIDN07 - TGTTTCGTTGATAGATTATACGGTAACGCTATCGCTTCCGTCAACAAGAAC -747
|||| | || || || ||||| | || ||||||||| || | ||
SEQIDN08 - TGTTTGTGCACAGGTTGTACGGCACTGCCATCGCTTCCGTTAATGAAAAT -750

SEQIDN07 - TTCCGCAACGACGCGGTCAAGCAGGAGGGATTCTATGGTGCAGGTGAAGT -797
| ||||| || | || || ||||| ||||||||||||| |||||
SEQIDN08 - TACCGCAACGATCCCGACAGGAAAGAGGGGTTCTATGGTGCAGGAGAAGT -800

SEQIDN07 - CAACTGTAAGTACCAGGACACC-----TACATCTTAG -829
|||| ||| |||| || |||||||||
SEQIDN08 - AAACGCGAGTTTGGGACTCCGAACAAACAGGAACAAGTACATCTTAG -850

SEQIDN07 - AACGCACTGGAATCGCCATGACAAATTACAACTACGATAACTTGAAGTAT -879
|||| ||||||||||||||||| ||||| ||||| |||||
SEQIDN08 - AACGAACTGGAATCGCCATGACAAATTACAATTATGACAACTATAACTAC -900

SEQIDN07 - AACCAGTGGGACCTTAGACCTCCGCATCATGATGGTGCCCTCAACCCAGA -929
|||||| || |||| |||| || | |||||
SEQIDN08 - AACCAGTCAGATCTTATTGTCCAGGATATCCT-----TCCGACCCGAA -944

SEQIDN07 - CTATTATATTCCAATGTACTACGCAGCACCTTGGTTGATCGTTAATGGAT -979
|| || ||||| ||||| ||||||||||||| | ||||| |||||
SEQIDN08 - CTTCTACATTCCCATGTATTTGCAGCACCTTGGGTAGTTGTTAAGGGAT -994

SEQIDN07 - GCGCCGGTACTTCGGAG---CAGTACTCGTATGGATGGTTCATGGACAAT -1026
|| || | || ||||||||||| ||||||| ||||| |||
SEQIDN08 - GCAGTGGCAACAGCGATGAACAGTACTCGTACGGATGGTTTATGGATAAT -1044

SEQIDN07 - GTCTCTCAATCTTACATGAATACTGGAGATACTACCTGGAATTCTGGACA -1076
|||| ||| ||||||||||||||||| ||||| ||||||| |||||
SEQIDN08 - GTCTCCCAAACCTTACATGAATACTGGTGGTACTTCTCGGAAGTGTGGAGA -1094

SEQIDN07 - AGAGGACCTGGCATAACATGGGCGCGCAGTATGGACCATTTGACCAACATT -1126

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      ||| || ||||| ||||| || |||| || ||||| ||||| |||||
SEQIDN08 - GGAGAACTTGGCATACATGGGAGCACAGTGCAGTCCATTGACCAACATT -1144

SEQIDN07 - TTGTTTACGGTGCTGGGGGTGGGATGGAATGTGTGGTCACAGCGTTCTCT -1176
      |||| || |||| ||| || ||| || || ||||| ||||| |||||
SEQIDN08 - TTGTGTATGGTGATGGAGATGGTCTTGAGGATGTTGTCCAAGCGTTCTCT -1194

SEQIDN07 - CTTCTACAAGGCAAGGAGTTCGAGAACCAAGTTCTCAACAAACGTTTCAGT -1226
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
SEQIDN08 - CTTCTGCAAGGCAAAGAGTTTGAGAACCAAGTTCTGAACAAACGTGCCGT -1244

SEQIDN07 - AATGCCTCCGAAATACGTCTTTGGTTTCTTCCAGGGTGTTCGGGACTT -1276
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
SEQIDN08 - AATGCCTCCGAAATATGTGTTTGGTTACTTTCAGGGAGTCTTTGGGATTG -1294

SEQIDN07 - CTTCTTGTGAGAGCGCATATGCCAGCAGGTGAGAACAACATCTCAGTC -1326
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
SEQIDN08 - CTTCTTGTGAGAGAGCAAAGACCAGAGGGTGGTAATAACATCTCTGTT -1344

SEQIDN07 - GAAGAAATTGTAGAAGGTTATCAAAACAACAATTTCCCTTTCGAGGGGCT -1376
      |||| |||| ||||| ||||| |||| |||| ||||| ||||| ||||| |||||
SEQIDN08 - CAAGAGATTGTGCAAGGTTACCAAAGCAATAACTTCCCTTAGAGGGGTT -1394

SEQIDN07 - CGCTGTGGACGTGGATATGCAAGACAACCTGCGGGTGTTCACCACGAAGG -1426
      || || || ||||| ||||| || ||||| ||||| ||||| ||||| |||||
SEQIDN08 - AGCCGTAGATGTGGATATGCAACAAGATTTGCGCGTGTTCACCACGAAGA -1444

SEQIDN07 - GCGAATTTTGGACCGCAAACAGGGTGGTACTGGCGGGGATCCAAACAAC -1476
      ||||| ||||| ||||| |||| |||| |||| |||| |||| |||| ||||
SEQIDN08 - TTGAATTTTGGACGGCAAATAAGGTAGGCACCGGGGAGACTCGAATAAC -1494

SEQIDN07 - CGATCGGTTTTGAATGGGCACATGACAAAGGCCTTGTTCAGACAAA -1526
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
SEQIDN08 - AAGTCGGTGTGTTGAATGGGCACATGACAAAGGCCTTGTATGTCAGACGAA -1544

SEQIDN07 - TATAACTTGCTTCCTGAGGAATGATAACGAGGGGCAAGACTACGAGGTCA -1576
      || ||||| |||| |||| || |||| |||| |||| |||| |||| ||||
SEQIDN08 - TGTTACTTGCTTCTTGAGAAACGACAACGGCGGGGAGATTACGAAGTCA -1594

SEQIDN07 - ATCAGACGTTAAGGGAGAGGCAGTTGTACCGAAGAAGCACTCCCTGACG -1626
      ||||| || ||||| || ||||| ||||| ||||| ||||| ||||| |||||
SEQIDN08 - ATCAGACATTGAGGGAGAAGGGTTGTACCGAAGAATGACTCACTGACG -1644

SEQIDN07 - GGTACGGATTTTGAATGACCGACGACGGCCCAGCGATGCGTACATCGG -1676
      || || || |||| |||| ||||| || ||||| ||||| ||||| |||||
SEQIDN08 - AACACTAATTCGGAACACCAACGACGGCCGAGCGATGCGTACATTGG -1694

SEQIDN07 - TCATCTGGACTATGGGGTGGAGTAGAATGTGATGCACTTTTCCCAGACT -1726
      ||||| ||||| || |||| || ||||| ||||| ||||| ||||| |||||
SEQIDN08 - ACATCTGGACTATGGTGGCGGAGGGAATTGTGATGCACTTTTCCCAGACT -1744

SEQIDN07 - GGGGACGGCCTGACGTGGCCGAATGGTGGGGAAATAACTATAAGAACTG -1776
      |||| || || || ||||| ||||| ||||| ||||| ||||| |||||
SEQIDN08 - GGGGTCGACCGGTGTGGCTGAATGGTGGGGTGATAACTACAGCAAGCTC -1794

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SEQIDN07 - TTCAGCATTGGTCTCGACTTCGTCTGGCAAGACATGACTGTTCCAGCAAT -1826
 |||| ||||||| || |||||||||||||||| ||||||| ||
 SEQIDN08 - TTCAAAATTGGTCTGGATTTCGTCTGGCAAGACATGACAGTTCCAGCTAT -1844

 SEQIDN07 - GATGCCGCACAAAATTGGCGATGACATCAATGTGAAACCGGATGGGAATT -1876
 |||||| |||||| |||||| | || || || | | |
 SEQIDN08 - GATGCCACACAAAGTTGGCGACGCAGTCGATACGAGATCACCTTACGGCT -1894

 SEQIDN07 - GGCCGAATGCGGACGATCCGTCCAATGGACAATACAACTGGAAGACGTAC -1926
 |||||||| | | ||||| || || |||| |||||| |||| | |||
 SEQIDN08 - GGCCGAATGAGAATGATCCTTCGAACGGACGATACAATTGGAAATCTTAC -1944

 SEQIDN07 - CATCCCCAAGTGCTTGTAACTGATATGCGTTATGAGAATCATGGTCGGGA -1976
 |||||| ||||| || ||||||||||||||| ||||||||||||| ||||
 SEQIDN08 - CATCCACAAGTTCTCGTAACTGATATGCGATATGAGAATCATGGAAGGGA -1994

 SEQIDN07 - ACCGATGGTCACTCAACGCAACATTTCATGCGTATACACTGTGCGAGTCTA -2026
 |||||| ||||||||||||| || |||||||| ||||| || | ||||
 SEQIDN08 - ACCGATGTTCACTCAACGCAATATGCATGCGTACACACTCTGTGAATCTA -2044

 SEQIDN07 - CTAGGAAGGAAGGGATCGTGAAAACGCAGACACTCTAACGAAGTTCCGC -2076
 | ||||||||||||| || || || |||||||||||||||||||||
 SEQIDN08 - CGAGGAAGGAAGGGATTGTTGCAATGCAGACACTCTAACGAAGTTCCGC -2094

 SEQIDN07 - CGTAGCTACATTATCAGTCGTGGTGGTTACATTGGTAACCAGCATTTCGG -2126
 || || || ||||||||||||| ||||||||| ||||||||| ||
 SEQIDN08 - CGCAGTTATATTATCAGTCGTGGAGGTTACATTGGCAACCAGCATTTTGG -2144

 SEQIDN07 - GGGTATGTGGGTGGGAGACAACTCTACTACATCAAACCTACATCCAAATGA -2176
 || ||||||||| ||||||||| | | || || |||||||||
 SEQIDN08 - AGGAATGTGGGTGGGAGACAACTCTCTCCCAAAGATACCTCCAAATGA -2194

 SEQIDN07 - TGATTGCCAACAATATTAACATGAATATGTCTTGCTTGCTCTCGTCGGC -2226
 |||| || |||| | ||||||| ||||||||| || || || ||
 SEQIDN08 - TGATCGCGAACATCGTCAACATGAACATGTCTTGCTTCCACTAGTTGGG -2244

 SEQIDN07 - TCCGACATTGGAGGATTCACCTCATACGACAATGAGAATCAGCGAACGCC -2276
 ||||||||||||| || || || || || | ||||
 SEQIDN08 - TCCGACATTGGAGGTTTACTTCGTATGA-----TGGACGAAACGT -2285

 SEQIDN07 - GTGTACCGGGGACTTGATGGTGAGGTATGTGCAGGCGGGCTGCCTGTTGC -2326
 |||| |||||| | |||| || | ||||||||| ||| | |
 SEQIDN08 - GTGTCCCGGGGATCTAATGGTAAGATTCTGTCAGGCGGGTTGCTTACTAC -2335

 SEQIDN07 - CGTGGTTCAGGAACCACTATGATAGGTGGATCGAGTCCAAGGACCACGGA -2376
 ||||||||| ||||||||| |||| | |||| |||| | ||||
 SEQIDN08 - CGTGGTTCAGAAACCACTATGGTAGGTTGGTCGAGGGAAGCAAGAGGGA -2385

 SEQIDN07 - AAGGACTACCAGGAGCTGTACATGTATCCGAATGAAATGGATACGTTGAG -2426
 || |||| || || ||||||||| | || |||| || |||||
 SEQIDN08 - AAATACTATCAAGAACTGTACATGTACAAGGACGAGATGGCTACATTGAG -2435

 SEQIDN07 - GAAGTTCGTTGAATTCGGTTATCGCTGGCAGGAAGTGTGTACACGGCCA -2476

|| ||| |||||||||||| |||||||||||| |||||||||||| ||
 SEQIDN08 - AAAATTCATTGAATTCCGTTACCGCTGGCAGGAGGTGTTGTACTGCTA -2485

 SEQIDN07 - TGTACCAGAATGCGGCTTTTCGGAAAGCCGATTATCAAGGCTGCTTCGATG -2526
 |||||||||||||||||| || |||||||||||||| |||| ||
 SEQIDN08 - TGTACCAGAATGCGGCTTTTCGGGAAACCGATTATCAAGGCAGCTTCCATG -2535

 SEQIDN07 - TACAATAACGACTCAAACGTTTCGCAGGGCGCAGAACGATCATTTCTTCT -2576
 ||| | ||||| ||||||||| | || ||| | || |||||||
 SEQIDN08 - TACGACAACGACAGAAACGTTTCGCGGCGCACAGGATGACCACTTCCTTCT -2585

 SEQIDN07 - TGGTGGACATGATGGATATCGCATTCTGTGCGCGCCTGTTGTGTGGGAGA -2626
 || ||||| |||||||||| ||| |||| || |||||||||||||||
 SEQIDN08 - CGGCGGACACGATGGATATCGTATTTTGTGTGCACCTGTTGTGTGGGAGA -2635

 SEQIDN07 - ATTCGACCGAACGCGAATTGTACTTGCCCGTGCTGACCCAATGGTACAAA -2676
 || | ||| ||||| |||||||||| |||||||||| |||||||||||
 SEQIDN08 - ATACAACCAGTCGCGATCTGTACTTGCCTGTGCTGACCAAATGGTACAAA -2685

 SEQIDN07 - TTCGGTCCCGACTTTGACACCAAGCCTCTGGAAGGAGCGATGAACGGAGG -2726
 ||||| || ||||| ||||||||| ||||| ||| ||| |||||
 SEQIDN08 - TTCGGCCCTGACTATGACACCAAGCGCCTGGATTCTGCGTTGGATGGAGG -2735

 SEQIDN07 - GGACCGAATTTACAACCTACCCTGTACCGCAAAGTGAATCACCAATCTTCG -2776
 || | ||| ||||| ||||| || ||||| || ||| || |||
 SEQIDN08 - GCAGATGATTAAGAACTATTCTGTGCCACAAAGCGACTCTCCGATATTTG -2785

 SEQIDN07 - TGAGAGAAGGTGCGATTCTCCCTACCCGCTACACGTTGAACGGTGAAAAC -2826
 |||| ||||| || |||||||||||||||||||||| ||||| |||
 SEQIDN08 - TGAGGGAAGGAGCTATTCTCCCTACCCGCTACACGTTGGACGGTTCGAAC -2835

 SEQIDN07 - AAATCATTGAACACGTACACGGACGAAGATCCGTTGGTGTTTGAAGTATT -2876
 || ||| |||||||||| ||| |||| |||||||||| |||||
 SEQIDN08 - AAGTCAATGAACACGTACACAGACAAAGACCCGTTGGTGTTTGAAGTATT -2885

 SEQIDN07 - CCCCTCGGAAACAACCGTGCCGACGGTATGTGTTATCTTGATGATGGCG -2926
 ||| || |||||||||||||||||||||||||||||||||||
 SEQIDN08 - CCCTCTTGGAACAACCGTGCCGACGGTATGTGTTATCTTGATGATGGCG -2935

 SEQIDN07 - GTGTGACCACCAATGCTGAAGACAATGGCAAGTTCTCTGTCGTCAAGGTG -2976
 || | || || ||||| ||| |||||| ||||||| ||||| ||
 SEQIDN08 - GTATTACTACAGATGCTGAGGACCATGGCAAATTCTCTGTTATCAATGTC -2985

 SEQIDN07 - GCAGCGGAGCAGGATGGTGGTACGGAGACGATAACGTTTACGAATGATTG -3026
 | ||| | || |||| |||| ||||| | |||| || |||||
 SEQIDN08 - GAAGCCTTACGGAAGGTGTTACGACGACGATCAAGTTGCGTATGACAC -3035

 SEQIDN07 - CTATGAGTACGTTTTCGGTGGACCGTTCTACGTTGAGTGCGCGGCGCTC -3076
 ||| | ||||| || | ||| || |||||||||| || |||
 SEQIDN08 - TTATCAATACGTATTTGATGGTCCATTCTACGTTCGAATCCGTAATCTTA -3085

 SEQIDN07 - AGTCGCCGTCGAACATCCACGTGTCTTCTGGAGCGGGTTCTCAGGACATG -3126
 || | || || || || |||||||||||||||||| |||||
 SEQIDN08 - CGACTGCATCAAAAATTAACGTGTCTTCTGGAGCGGGTGAAGAGGACATG -3135

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SEQIDN07 - AAGGTGAGCTCTGCCACTTCCAGGGCTGCGCTGTTCAATGACGGGGAGAA -3176
          |  || ||||| | || ||||| || ||||| ||| || |
SEQIDN08 - ACACCGACCTCTGCGAACTCGAGGGCAGCTTTGTTCACTGATGGAGGTGT -3185

SEQIDN07 - CGGTGATTCTGGGTTGACCAGGAGACAGATTCTCTGTGGCTGAAGTTGC -3226
          || || | ||||| |||| | || || ||||| ||||| |||||
SEQIDN08 - TGGAGAATACTGGGCTGACAATGATACGTCTTCTCTGTGGATGAAGTTGC -3235

SEQIDN07 - CCAACGTTGTTCTCCCGGACGCTGTGATCACAATTACCTAA -3267
          | ||| | |||| | ||||| ||||| || ||||| ||
SEQIDN08 - CAAACCTGGTTCTGCAAGACGCTGTGATTACCATTACGTAG -3276

```

Identity : 2550 (78.05%)

Number of gaps inserted in SEQIDN07: 3

Number of gaps inserted in SEQIDN08: 2

===03-MAY-2001=====NALIGN=====PC/GENE===

===03-MAY-2001=====NALIGN=====PC/GENE===

* ALIGNMENT OF TWO NUCLEOTIDE SEQUENCES. *

The two sequences to be aligned are:

SEQIDN07.

Total number of bases: 3267.

SEQIDN09.

Total number of bases: 3201.

Open gap cost : 50

Unit gap cost : 20

The character to show that two aligned residues are identical is '|'

```
SEQIDN07 - ATGTTTTCAACCCCTTGCGTTTGTGCGACCTAGTGCCTGGGAGCCAGTAC -50
          |||      |      ||      ||      |      |||
SEQIDN09 - ATGGCAGGATTTTCTGATCCTCTCAACTTTGCAAAGCAGAAGACTACTA -50

SEQIDN07 - CTTCGTAGGGGCGGAGGTCAGGTCAAATGTTTCGTATCCATTCCGCTTTTC -100
          |  |||  |  ||      |      |      |||  |  |
SEQIDN09 - CAGTGTTGCGCTAGACTGGAAGGGCCCTCAAAAAATCATTGGAGTAGACA -100

SEQIDN07 - CAGCTGTGCACACAGCTACTCGAAAAACCAATCGCCTCAATGTATCCATG -150
          |  ||  |  |      ||      |||  |  |||  |  ||
SEQIDN09 - CTACTCCTCCAAAGAGCACCAAGTTCCCCAAAACTGGCATGGAG---TG -147

SEQIDN07 - ACCGCATTGTCCGACAAACAAACGGCTACTGCGGGTAGTACAGACAATCC -200
          |  |  |  |||  |  ||      ||  |||  |  ||
SEQIDN09 - AACTTGAGATTGATGATGGGACTTTAGGTGTGGTTCAAGTTCATTAGGCC -197

SEQIDN07 - GGACGGTATCGACTACAAGACCTACGATTACGTCGGAGTATGGGGTTTCA -250
          |  |||  |  |      |||  |  ||      |  |
SEQIDN09 - GTGCGTTTGGAGGGTTAGATACGACCCTGGTTTCAAGACCTCTGACGAGT -247

SEQIDN07 - GCCCCCTCTCCAACACGAACTGGTTTGCTGCCGGCTCTTCTACCCCGGGT -300
          ||  |||  |||      |  |  |  |  |
SEQIDN09 - ATGGTGATGAGAATACGAGGACAATTGTGCAAGATTATATGAGTACTCTG -297

SEQIDN07 - GGCATCACTGATTGGACGGCTACAATGAATGTCAACTTCGACCGTATCGA -350
          |  |  |  ||  |||  |      |      ||
SEQIDN09 - AGTAATAAATTGGATACTTATAGAGGTCTTACGTGGGAAACCAAGTGTGA -347

SEQIDN07 - CAATCCGTCCATCACTGTCCAGCATCCCGTTCAGGTTCAAGTTCACGTCAT -400
          ||  ||  |  |  |  |  |  |  |  |  |  |  |
SEQIDN09 - GGATTCCGGG-AGATTTCTTTACCTTCTCATCAAGTCAACGCCGTTGAA -396

SEQIDN07 - ACAACAACAACAGCTACAGGGTTCGCTTCAACCCTGATGGCCCTATTTCGT -450
          |  |  |  |  |  |  |  ||  |  ||  |  |||
SEQIDN09 - AAATC--CGAGCGGACCCGCAACAAGGTCGGCGATGGCCTCAGAATTCAC -444
```


SEQIDN07 - GATGTGACTCGTGGGCCTATCCTCAAGCAGCAACTAGATTGGATTCGAAC -500
 || | ||| | ||| |
 SEQIDN09 - CTATGGAAAAGCCCTTTCGCATCCAAGTAGTGCACCTTGACCCCTTT -494

SEQIDN07 - GCAGGAGCTGTCAGAGGGATGTGATCCCGGAATGACTTTCACATCAGAAG -550
 | |||| | || | | |
 SEQIDN09 - GAAGGATCCTTACCCCATTCCAAATGTAGCCGCAGCCGAAGCCCGTGTGT -544

SEQIDN07 - GTTCTTGACTTTTGAGACCAAGGATCTAAGCGTCATCATCTACGGAAT -600
 | | || | || | ||| |
 SEQIDN09 - CCGACAAGGTCGTTTGGCAAACGTCTCCAAGACATTCAGAAAGAACCTG -594

SEQIDN07 - TTCAAGACCAGAGTTACGAGAAAGTCTGACGGCAAGTCATCATGGAAAA -650
 | | | |||| | | ||| | ||
 SEQIDN09 - CATCCGCAACACAAGATGCTAAAGGATACAGTTCTTGACATTGTCAAACC -644

SEQIDN07 - TGATGAAGTTGGAAGTCATCGTCCGGGAACAAGTCCGGGGATTGATGT -700
 || | | | || | | | | | | | | | |
 SEQIDN09 - TGGACATGGCGAGTATGTGGGGTGGGAGAGATGGGAGGTATCCAGTTTA -694

SEQIDN07 - TCGTTGATAGATTATACGGTAACGCTATCGTTCCGTCAACAAGAACTTC -750
 | | | | | | | | | | | | | | | | | |
 SEQIDN09 - TGAAGGAGCCAACATTCATGAACTATTTAACTTCGACAATATGCAATAC -744

SEQIDN07 - CGCAACGACCGGTCAAGCAGGAGGGATTCTATGGTGCAGGTGAAGTCAA -800
 | | | | | | | | | | | | | | | |
 SEQIDN09 - CAGCAAGTCTATGCCAAGGTGCTCTCGATTCTCGCGAG-----CCA -786

SEQIDN07 - CTGTAAGTACCAGGACACCTACATCTTAGAACGCACTGGAATCGCCATGA -850
 |||| | | | | | |||| | | | | | | | | |
 SEQIDN09 - CTGTACCACTCGGATCCCTTCTATCTTGATGTGAACTCAACCCGGAGCA -836

SEQIDN07 - CAAATTACAACACGATAACTTGAAGTATAACCAAGTGGGACCTTAGACCT -900
 || | | | | | | | | | | | | | | | | | | | |
 SEQIDN09 - CAAGA-ATATCAGGCAACCTTTATCGATAACTACTCTCAAATT-GCCAT -884

SEQIDN07 - CCGCATCATGATGGTGCCTCAACCCAGACTATTATATTCCAATGTACTA -950
 | | | | | |||| | | | | | | | | | |
 SEQIDN09 - CGACTTTGGAAAGACCAACTCAGGCTACATCAAGCTGGGAACCAGGTATG -934

SEQIDN07 - CGCAGCACCTTGGTTGATCGTTAATGGATGCGCCGGTACTTCGGAGCAGT -1000
 | | || | | | | | | |||| | | | | |
 SEQIDN09 - GTGGTATCGATTGTTACGGTATCAGTGCAGGATACGGTCCCG-GAAATTGT -983

SEQIDN07 - ACTCGTATGGATGGTTCATGGACAATGTCTCTCAATCTTACATGAATACT -1050
 || | | | | | | | | | | | | | | | | |
 SEQIDN09 - ACGACTTTATACAGGTCTTGTTGGACGTTCAAAGTTGAAGCCCAGATATA -1033

SEQIDN07 - GGAGATACTACCTGGAATTCTGGACAAGAGGACCTGGCATACATGGGCGC -1100
 || | | || | | | | | | | | | | |
 SEQIDN09 - TTCTCGGGGCCCATCAAGCCTGTT-ATGGATACCAACAGGAAAGTGACTT -1082

SEQIDN07 - GCAGTATGGACATTTGACCAACATTTTGTTTACGGTGCTGGGGGTGGGA -1150

SEQIDN09	-	GTATTCTGTGGTCCAGCAGTACCGTGACTGTAAATTTCCACTTGACG	GGA	-1132					
SEQIDN07	-	TGGAATGTGTGGTCACAGCGTTCTCTCTTCTACAAGGCAAGGAGTT	TCGAG	-1200					
SEQIDN09	-	TTCACGTCGATGTCGATGTTTCAGGACGGCTTCAGAACTTTCACCAC	CAAC	-1182					
SEQIDN07	-	AACCAAGTTCTCAACAAACGTTTCAGTAATGCCTCCGAAATACGTC	TTTGG	-1250					
SEQIDN09	-	CCACACACTTTCCCTAACCCCAAAGAGATGTTTACTA	ACTTGAGGAATAA	-1232					
SEQIDN07	-	TTTCTTCCAGGGTGTTTTCGGGACTTCTTCCTTGTTGAGAGCGCAT	ATGC	-1300					
SEQIDN09	-	TGGAATCAAGTGCTCCACCAATATCACTCCTGTTATCAGCATTA	ACAACA	-1282					
SEQIDN07	-	CAGCAGGTGAGAACAACATCTCAGTCGAAGAAATTGTAGAAGGTT	TATCAA	-1350					
SEQIDN09	-	GAGAGGGTGGATACAGTACCCTCCTTGAGGGAGTTGACAAAAA	ATACTTT	-1332					
SEQIDN07	-	AACAACAATTTCCCTTTTCGAGGGGCTCGCTGTGGACGTGGATAT	GCAAGA	-1400					
SEQIDN09	-	ATCATGGACGACAGATATACCGAGGGAACAAGTGGGAATGCGA	AAGGATGT	-1382					
SEQIDN07	-	CAACTTGCGGGTGTTTACCACGAAGGGCGAATTTTGACCGCAA	ACAGGG	-1450					
SEQIDN09	-	TCGGTACATGTACTACGGTGGTGGTAATAAGGTTGAGGTCGAT	CTTAATG	-1432					
SEQIDN07	-	TGGGTACTGGCGGGGATCCAAACAACCGATCGGTTTTTGAATGG	GCACAT	-1500					
SEQIDN09	-	ATGTTAATGGTCGGCCAGACTTTAAAGACA	ACTATGACTTCCCCGCGAAC	-1482					
SEQIDN07	-	GACAAAGGCCCTTGTTTGTGACAGCAAATATAACTTGCTTCTG	AGGAATGA	-1550					
SEQIDN09	-	TTCAACAGCAAACAATACCCCTATCATGGTGGTGTGAGCTAC	GGTTATGG	-1532					
SEQIDN07	-	TAACGAGGGGCAAGACTACGAGGTCAATCAGACGTTAAGGGAG	AGGCAGT	-1600					
SEQIDN09	-	GAACGGTAGTGCAGGTTTTTACCCGGACCTCAACAGAAAGG	AGGTTTCGTA	-1582					
SEQIDN07	-	TGTACACGAAGAACGACTCCCTGACGGGTACGGATTTTGAATG	ACCGAC	-1650					
SEQIDN09	-	TCTGGTGGGAATGCAGTACAAGTATCTCTTCGATATGGGACT	GGAATTT	-1632					
SEQIDN07	-	GACGGCCCCAGCGATGCGTACATCGGTCATCTGGACTATGGGG	TGGAGT	-1700					
SEQIDN09	-	GTGTGGCA-AGACATGACTACCCAGCAATCCACACATCATATG	GAGACA	-1681					
SEQIDN07	-	AGAATGTGATGCACTTTTCCCAGACTGGGGACGGCTGACGTGG	CCGAAT	-1750					
SEQIDN09	-	TGAAAGGGTTGCCACCCGTCTACTCGTCACCTCAGACTCCGT	CACCAAT	-1731					
SEQIDN07	-	GGTGGGGAAATAACTATAAGAACTGTTTCAGCATTGGTCTCG	ACTTCGTC	-1800					
SEQIDN09	-	GCCTCTGAGAAAAAGCTCGCAATTGAACTTGGGCTCTCTACT	CCTACAA	-1781					

SEQIDN07 - TGGCAAGACATGACTGTTCCAGCAATGATGCCGCACAAAATTGGCGATGA -1850
 | | | | | | | | | | | | | |
 SEQIDN09 - TCTCCACAAAGCAACTTGGCATGGTCTTAGTCGTCTCGAATCTCGTAAGA -1831

SEQIDN07 - CATCAATGTGAAACCGGATGGGAATTGGCCGAATGCCGACGATCCGTCCA -1900
 | | | | | | | | | | | | | |
 SEQIDN09 - ACAAACGAAACTTCATCCTCGGGCGTGGAAG--TTATGCCGAGCCTATC -1879

SEQIDN07 - ATGGACAATACAACTGGAAGACGTACCATCCCCAAGTGCTTGTAACTGAT -1950
 | | | | | | | | | | | | | |
 SEQIDN09 - GTTTTGCTGGTCTCTGGACTGGGGATAATGCAAGTAACTGGGAATTCTGG -1929

SEQIDN07 - ATGCGTTATGAGAATCATGGTCGGGAACCGATGGTCACTCAACGCAACAT -2000
 | | | | | | | | | | | | | |
 SEQIDN09 - AAGATATCGGTCTCTCAAGTTCTTTCTCTGGGCCTCAATGGTGTGTGCAT -1979

SEQIDN07 - TCATGCGTATACACTGTGCGAGTCTACTAGGAAGGAAGGGATCGTGAAAA -2050
 | | | | | | | | | | | | | |
 SEQIDN09 - CGCGGGGTCTGATACGGGTGGTTTT-----GAACCCTACCGTGATGCAAA -2024

SEQIDN07 - ACGCAGACACTCTAACGAAGTTCGCGCGTAGCTACATTATCAGTCGTGGT -2100
 | | | | | | | | | | | | | |
 SEQIDN09 - TGGGGTCGAGGAGAAATACTGTAGCCAGAGCTAC-TCATCAGGTGGTAT -2073

SEQIDN07 - GGTTACATTGGTAACCAGCATTTTCGGGGGTATGTGGGTGGGAGACAACTC -2150
 | | | | | | | | | | | | | |
 SEQIDN09 - ACTGGTTCATTCCCTCTTGCCGTGGCTCAGGAACCATTATGTCAAAAAGGA -2123

SEQIDN07 - TACTACATCAAACCTACATCCAAATGATGATTGCCAACAAATATTAACATGA -2200
 | | | | | | | | | | | | | |
 SEQIDN09 - CAGGAAATGGTTCCAGGAACCATACTCGTACCCCAAGCATCTTGAAACCC -2173

SEQIDN07 - ATATGTCTTGCTTGCCTCTCGTCGGCTCCGACATTGGAGGATTACCTCA -2250
 | | | | | | | | | | | | | |
 SEQIDN09 - ATCCAGAACTCGCAGACCAAGCATGGCTCTATAATCCGTTTTGGAGATC -2223

SEQIDN07 - TACGACAATGAGAATCAGCGAACGCCGTGTACCGGGGACTTGATGGTGAG -2300
 | | | | | | | | | | | | | |
 SEQIDN09 - TGTAGGTACTATGTGGAGCTTAGATACTCCCTCATCCAACACTTTACGA -2273

SEQIDN07 - GTATGTGCAGGCGGGCTGCCTGTTGCCGTGGTTCAGGAACCACTATGATA -2350
 | | | | | | | | | | | | | |
 SEQIDN09 - CTGCATGTTTCAAAACGTAGTCGACGGTATGCCAATCACCAGATCTATGC -2323

SEQIDN07 - GGTGGATCGAGTCCAAGGACCACGGAAGGACTACCAGGAGCTGTACATG -2400
 | | | | | | | | | | | | | |
 SEQIDN09 - TCTTGACCGATACTGAGGATACCACCTTCTTCAACGAGAGCCAAAAGTTC -2373

SEQIDN07 - TATCCGAATGAA-ATGGATACGTTGAGGAAGTTCGTTGAATTCCGTTATC -2449
 | | | | | | | | | | | | | |
 SEQIDN09 - CTCGACAACCAATATATGGCTGGTGACGACATTCTTGTTGCACCCATCCT -2423

SEQIDN07 - GCTGGCAGGAAGTGTGTACACGGCCATGTACCAGAATGCGGCTTTCGGA -2499

SEQIDN09 - CCACAGTCGCAAAGAAATTCCAGGCGAAAACAGAGATGTCTATCTCCCTC -2473
 | | | | | | | | |
 SEQIDN07 - AAGCCGATTATCAAGGCTGCTTCGATGTACAATAACGACTCAAACGTTTCG -2549
 | | | | | | | | |
 SEQIDN09 - TTTACCACACCTGGTACCCCTCAAATTTGAGACCATGGGACGATCAAG-G -2522
 SEQIDN07 - CAGGGCGCAGAACGATCATTTCTTCTTGGTGGACATGATGGATATCGCA -2599
 | | | | | | | | |
 SEQIDN09 - AGTCGCTTTGGGGAATCCTGTGCAAGGTGGTAGTGTCAATTATACTG -2572
 SEQIDN07 - TTCTGTGCGCGCCTGTTGTGTGGGAGAATTCGACCGAACGGAATTGTAC -2649
 | | | | | | | | |
 SEQIDN09 - CTAGGATTGTTGCACCCGAGGATTATAATCTCTTCCACAGCG--TGGTAC -2620
 SEQIDN07 - TTGCCCCGTCTGACCCAATGGTACAAATTCGGTCCCGACTTTGACACCAA -2699
 | | | | | | | | |
 SEQIDN09 - CAGTCTACGTTAGAGAGGGTGCCATCATCCCGCAAATCGAAGTACGCCAA -2670
 SEQIDN07 - GCCTCTGGAAGGAGCGATGAACGGAGGGGACCGAATTTACAACCTACCCTG -2749
 | | | | | | | | |
 SEQIDN09 - TGGACTGGCCAGGGGGGAGC-CAACCGCATCAAGTTCAACATCTACCCTG -2719
 SEQIDN07 - TACCGCAAAGTGAATCACCAATCTTCGTGAGAGAAGGTGCGATTCTCCCT -2799
 | | | | | | | | |
 SEQIDN09 - GAAAGGATAAGGAGTACTGTACCTATCTTGATGATGGTGTTAGCCGTGAT -2769
 SEQIDN07 - ACCCGCTACACGTTGAACGGTGAAAACAAATCATTGAACACGTACACGGA -2849
 | | | | | | | | |
 SEQIDN09 - AGTGCGCC-----GGAAGACCTCCACAGTACAAAGAGACCCA -2807
 SEQIDN07 - CGAAGATCCGTTGGTGTGTTGAAGTATCCCCCTCGGAAACAACCGTGCCG -2899
 | | | | | | | | |
 SEQIDN09 - CGAACA---GTCGAAGGTTGAAGGCGCGGAAATCGCAAAGCAGATTGGAA -2854
 SEQIDN07 - ACGGTATGTGTTATCTTGATGATGGCGGTGTGACCACCAATGCTGAAGAC -2949
 | | | | | | | | |
 SEQIDN09 - AGAAGACGGGTTACAACATCTCAGGA-----ACCGACCCAGAAGCA -2895
 SEQIDN07 - AATGGCAAGTTCTCTGTCTCAAGGTGGCAGCGGAGCAGGATGGTGGTAC -2999
 | | | | | | | | |
 SEQIDN09 - AAGGGTTATCACCGCAAAGTTGCTGTACACAAACGTCAAAGACAAGAC -2945
 SEQIDN07 - GGAGACGATAACGTTTACGAATGATTGCTATGAGTACGTTTTCGGTGGAC -3049
 | | | | | | | | |
 SEQIDN09 - GCGTACTGTCACTATTGAGCCAAAACACAATGGATACGACCCTTCCAAAG -2995
 SEQIDN07 - CGTTCTACGTTTCGAGTGCGCGGCGCTCAGTCGCCGTGGAACATCCACGTG -3099
 | | | | | | | | |
 SEQIDN09 - AGGTGGGTGATTATTATACCATCATTCTTTGGTACGCA-----CCAGGTT -3040
 SEQIDN07 - TCTTCTGGAGCGGGTTCTCAGGACATGAAGGTGAGCTCTGCCACTTCCAG -3149
 | | | | | | | | |
 SEQIDN09 - TCGATGGCAGCATCGTC---GATGTGAGCAAGACGACTGTGAATGTTGA -3086

SEQIDN07 - GGCTGCGCTGTTCAATGACGGGGAGAACGGTGATTTCTGGGTTGACCAGG -3199
|| || || | | | | | | | |
SEQIDN09 - GGGTGGGTGGAGCACCAAGTTTATAAGAACTCCGATTACATACGGTTG -3136

SEQIDN07 - AGACAGATTCTCTGTGGCTGAAGTTGCCCAACGTTGTTCTCCCGGACGCT -3249
| || | | || | | | | | | |
SEQIDN09 - TTATCGACGTGAAGGAGGTGATCGGTACCACAAAGAGCGTCAAGATCACA -3186

SEQIDN07 - GTGATCACAATTACCTAA -3267
|| | ||
SEQIDN09 - TG---TACTGCCGCTTAA -3201

Identity : 1108 (34.61%)

Number of gaps inserted in SEQIDN07: 1

Number of gaps inserted in SEQIDN09: 21

===03-MAY-2001=====NALIGN=====PC/GENE===

==03-MAY-2001=====NALIGN=====PC/GENE==

* ALIGNMENT OF TWO NUCLEOTIDE SEQUENCES. *

The two sequences to be aligned are:

SEQIDN07.

Total number of bases: 3267.

SEQIDN010.

Total number of bases: 3213.

Open gap cost : 50

Unit gap cost : 20

The character to show that two aligned residues are identical is '|'

```
SEQIDN07 - ATGTTTCAACCCTTGCCTTTGTGCGACCTAGTGCCTGGGAGCCAGTAC -50
          |||      |      ||      |||      |      |||      |      |||
SEQIDN010 - ATGGCAGGATTA--TCCGACCCTCTCAATTCTGCAAAGCAGAGGACTAC -48

SEQIDN07 - CTTCGTAGGGGCGGAGGTCAGGTCAAATGTTTCGTATCCATTCCGCTTTTC -100
          |      |      |||      |      |      |      |      |||||
SEQIDN010 - TACGCTGCTGCCAAAGGCTGGAGTGGCCCTCAGAAGATCATTCGCTATGA -98

SEQIDN07 - CAGCTGTGCACACAGCTACTCGAAAACCAATCGCCTCAATGTATCCATG -150
          |      |||      |      |      |      |      |      |||      |
SEQIDN010 - CCA-----GACCCCTCCTCAGGGTACAAAAGATCCGAAAAGCTGGCATGC -143

SEQIDN07 - ACCGCATTGTCCGACAAACAAACGGCTACTGCGGGTAGTACAGACAATCC -200
          |      |||      |      |      ||      |||      |||||      ||
SEQIDN010 - GGTAACCTTCCTTTCGATGACGGGACTATGTGTGTAGTGCAATTTCGTCA -193

SEQIDN07 - GGACGGTATCGACTACAAGACCTACGATTACGTCCGAGTATGGGGTTTCA -250
          |      |      |      |      |      |||      |||      |      ||
SEQIDN010 - GACCCTGT--GTTTGGAGGGTTAGATATGACCCAGTGTCAAGACTTCTG -241

SEQIDN07 - GCCCCCTCTCCAACACGAAGTGGTTTGCTGCCGGCTCTTCTACCCCGGGT -300
          |      |      |||      |      |      |      |      |||      |
SEQIDN010 - ATGAGTACGGCGATGAGAA----TACGAGGACTATTGTACAAGACTACAT -287

SEQIDN07 - GGCATCACTGATTGGACGGCTACAATGAATGTCAACTTCGACCGTATCGA -350
          |      |      |||      |||||      |      |      |      |      ||
SEQIDN010 - GACTACTCTGTTGAAACTTGGACATTTTCAGAGGTCTTACGTGGGTTT -337

SEQIDN07 - CAATCCGTCCATCACTGTCCAGCATCCCGTTCAGGTTCAAGTACGTCAT -400
          |      |      ||      ||      |      |      |||      |||
SEQIDN010 - CTACGTTGGAGGA---TTCGGGCGAGTACTACACCTTCAAGTCCGAAGTC -384

SEQIDN07 - ACAACAACAACAGCTACAGGGTTCGCTTCAACCCTGATGGCCCTATTTCGT -450
          ||      |      |||      |      ||      |||      |||      |
SEQIDN010 - ACTGCCGTGGACGAAACCGAACGGACTCGAAACAAGGTCGGCGACGGCCT -434
```

SEQIDN07 - GATGTGACTCGTGGGCCTATCCTCAAGCAGCAACTAGATTGGATTGGAAC -500
 | | | | | | | | | | | | | |
 SEQIDN010 - CAAGATTACCTATGGAAAAATCCCTTTTCGCATCCAG---GTAGTGCCTC -481

SEQIDN07 - GCAGGAGCTGTCAGAGGGATGTGATCCCGGAATGACTTTCACATCAGAAG -550
 | | | | | | | | | | | | | |
 SEQIDN010 - TCTTGACCCCCTGGTGGACCCTTTCCCC--ATTCCCAACGTAGCCAATG -529

SEQIDN07 - GTTCTTGACTTTTGAGACCAAGGATCTAAGCGTCATCATCTACGAAAT -600
 | | | | | | | | | | | | | |
 SEQIDN010 - CCACAGCCCGTGTGGCCGACAAGGTTGTTTGGCAGACGTCCCCGAAGACG -579

SEQIDN07 - TTCAAGACCAGAGTTACGAGAAAGTCTGACGGCAAGGTCATCATGGAAAA -650
 | | | | | | | | | | | | | |
 SEQIDN010 - TTCAGGAAAACTTGCATCCGAGCATAAGATGTTGAAGGATACAGTTCT -629

SEQIDN07 - TGATGAAGTTGGAAGTGCATCGTCCGGGAACAAGTCCGGGGATTGATGT -700
 | | | | | | | | | | | | | |
 SEQIDN010 - TGATATTATCAAGCCGGGACGAGAGTATGTGGGTGGGGAGAGATGG -679

SEQIDN07 - TCGTTGATAGATTATACGGTAACGCTATCGCTTCCGTCAACAAGAACTTC -750
 | | | | | | | | | | | | | |
 SEQIDN010 - GAGGCATCGAGTTTATGAAGGAGCCAACATTCATGAATTATTCAACTTT -729

SEQIDN07 - CGCAACGACGCGGTCAAGCAGGAGGGATTCTATGGTGCAGGTGAAGTCAA -800
 | | | | | | | | | | | | | |
 SEQIDN010 - GACAATATGCAATATCAGCAGGTCTATGCACAAGGCGCTCTTGATAGTCG -779

SEQIDN07 - CTGTAAGTACCAGGACACCTACATCTTAGAACGCACTGGAATCGCCATGA -850
 | | | | | | | | | | | | | |
 SEQIDN010 - TGAGCCGTTGTATCACTCTGATCCCTTCTATCTCGACGTGAACTCCAACC -829

SEQIDN07 - CAAATTACAACCTACGATAACTTGAAGTATAACCAAGTGGGACCTTAGACCT -900
 | | | | | | | | | | | | | |
 SEQIDN010 - CAGAGCACAAGAACATTACGGCAACCTTTATCGATAACTACTCTCAGATT -879

SEQIDN07 - CCGCATCATGATGGTGCCTCAACCCAGACTATTATATTCCAATGTACTA -950
 | | | | | | | | | | | | | |
 SEQIDN010 - GCCATCGACTTTGGGAAGACCAACTCAGGCTAC-ATCAAGCTGGGTACCA -928

SEQIDN07 - CGCAGCACCTTGGTTGATCGTTAATGGATGCGCCGTAATTCGGAGCAGT -1000
 | | | | | | | | | | | | | |
 SEQIDN010 - GGTATGGCGGTA-TCGATTGTTACGGTATCAGCGGGATACGGTCCCGGA -977

SEQIDN07 - ACTCGTATGGATGGTTCATGGACAATGTCTCTCAATCTTACATGAATACT -1050
 | | | | | | | | | | | | | |
 SEQIDN010 - GATTGTGCGACTTTATACTGGACT-TGTTGGGCGTTCCAAGTTGAAGCCC -1026

SEQIDN07 - GGAGATACTACCTGGAATTCTGGACAAGAGGACCTGGCATACTGGGCGC -1100
 | | | | | | | | | | | | | |
 SEQIDN010 - AGGTATATTCTCGGAGCCCAAGCTTGTATGGATACCAGCAGGAAAG -1076

SEQIDN07 - GCAGTATGGACCATTTGACCAACATTTTGTTTACGGTCTGGGGGTGGGA -1150

SEQIDN010 - TGACTTGCATGCTGTTGTTTCAGCAGTACCGTGACAC----CAAGTTTCCG -1122
 | | | | | | | | | |
 SEQIDN07 - TGGAATGTGTGGTCACAGCGTTCTCTTCTACAAGGCAAGGAGTTCGAG -1200
 | | | | | | | | | |
 SEQIDN010 - CTTGATGGGTTCATGTCGATGTCGACTTTCAGGACAATTCAGAACGTT -1172
 | | | | | | | | | |
 SEQIDN07 - AACCAAGTTCTCAACAAACGTTTCAGTAATGCCTCCGAAATACGTCTTTGG -1250
 | | | | | | | | | |
 SEQIDN010 - TACCACTAACCCGATTA-CGTTCCCTAATCCCAAAGAAATGTTTACCAA- -1220
 | | | | | | | | | |
 SEQIDN07 - TTTCTTCAGGGTGTTCGCGGACTTCTCCTTGTTGAGAGCGCATATGC -1300
 | | | | | | | | | |
 SEQIDN010 - TCTAAGGAACAATGGAATCAAGTGTTCCACCAACATCACCCCTGTTATCA -1270
 | | | | | | | | | |
 SEQIDN07 - CAGCAGGTGAGAACACATCTCAGTCGAAGAAATTGTAGAAGGTTATCAA -1350
 | | | | | | | | | |
 SEQIDN010 - GTATCAGAGATCGCCGAATGGGTACGTACCCTCAATGAGGGATATGAT -1320
 | | | | | | | | | |
 SEQIDN07 - AACAACAATTTCCCTTTCGAGGGGCTCGCTGTGGACGTGGATATGCAAGA -1400
 | | | | | | | | | |
 SEQIDN010 - AAAAAGTACTTCATCATGGATGACAGATATACCGAGGGGACAAGTGGGGA -1370
 | | | | | | | | | |
 SEQIDN07 - CAACTTGCGGGTGTTCACCACGAAGGGCGAATTTTGACCGCAAACAGGG -1450
 | | | | | | | | | |
 SEQIDN010 - CCCGCAAAATGTTGATACTCTTTTACGGCGGTGGGAACCCGTTGAGG -1420
 | | | | | | | | | |
 SEQIDN07 - TGGGTACTGGCGGGGATCCAAACAACCGATCGGTTTTGAATGGGCACAT -1500
 | | | | | | | | | |
 SEQIDN010 - TTAACCCTAATGATGTTTGGGCTCGGCCA-----GACTTTGGAGAC -1461
 | | | | | | | | | |
 SEQIDN07 - GACAAAGGCCTTGTGTCAGACAAATATACTTGCTTCCTGAGGAATGA -1550
 | | | | | | | | | |
 SEQIDN010 - AATTATGACTTCCTACGAACTTCAACTGCAAAGACTACCCCTATCATGG -1511
 | | | | | | | | | |
 SEQIDN07 - TAACGAGGGGCAAGACTACGAGGTCAATCAGACGTTAAGGGAGAGGCAGT -1600
 | | | | | | | | | |
 SEQIDN010 - TGGTGTGAGTTACGGATATGGGAATGGCACTCCAGGTTACTACCCTGACC -1561
 | | | | | | | | | |
 SEQIDN07 - TGTACACGAAGAACGACTCCCTGACGGGTACGGATTTTGAATGACCGAC -1650
 | | | | | | | | | |
 SEQIDN010 - TTAACAGAGAGGAGG--TTCGTATCTGGTGGGGATTGCAGTACGAGTATC -1609
 | | | | | | | | | |
 SEQIDN07 - GACGGCCCCAGCGATGCGTACATCGGTCATCTGGACTATGGGGGTGGAGT -1700
 | | | | | | | | | |
 SEQIDN010 - TCTTCAATATGGGACTAGAGTTGTATGGCAAGATATGACAACCCAGCG -1659
 | | | | | | | | | |
 SEQIDN07 - AGAATGTGATGCACTTTTCCAGACTGGGGACGGCCTGACGTGGCCGAAT -1750
 | | | | | | | | | |
 SEQIDN010 - ATCCATTTCATATGGAGACATGAAAGGGTTGCCACCCGTCTGCTCGT -1709
 | | | | | | | | | |
 SEQIDN07 - GGTGGGGAAATAACTATAAGAAACTGTTTCAGCATTGGTCTCGACTTCGTC -1800
 | | | | | | | | | |
 SEQIDN010 - CACCGCCGACTCAGTTACCAATGCCTCTGAGAAAAAGCTCGCAATTGAAA -1759
 | | | | | | | | | |

SEQIDN07 - TGGCAAGACATGACTGTTCCAGCAATGATGCCGCACAAAATTGGCGATGA -1850
 | | | | | | | | | |
 SEQIDN010 - GTTGGGCTCTTTACTCCTACAACTCCATAAAGCAACCTTCCACGGTCTT -1809

SEQIDN07 - CATCAATGTGAAACCGGATGGGAATTGGCCGAATGCGGACGATCCGTCCA -1900
 | | | | | | | | | | | | | |
 SEQIDN010 - GGTCTGCTTGTAGTCTCGTAAGAACAAACGTAACCTC-----ATCCTCGGA -1854

SEQIDN07 - ATGGACAATACAACCTGGAAGACGTACCATCCCCAAGTGCTTGTAACATGAT -1950
 | | | | | | | | | | | | | |
 SEQIDN010 - CGTGGTAGTTACGCCGGTGCCTATCGTTTTGCTGGTCTCTGGACTGGAGA -1904

SEQIDN07 - ATGCGTTATGAGAATCATGGTCGGGAACCGATGGTCACTCAACGCAACAT -2000
 | | | | | | | | | | | | | |
 SEQIDN010 - TAACGCAAGTACGTGGGAATTCTGGAAGATTTCGGTCTCCCAAGTTCTTT -1954

SEQIDN07 - TCATGCGTATACACTGTGCGAGTCTACTAGGAAGGAAGGGATCGTGAAA -2050
 | | | | | | | | | | | | | |
 SEQIDN010 - CTCTAGGTCTCAATGGTGTGTGTATAGCGGGTCTGATACGGGTGGTTTT -2004

SEQIDN07 - ACGCAGACACTCTAACGAAGTCCGCCGTAGCTACATTATCAGTCGTGGT -2100
 | | | | | | | | | | | | | |
 SEQIDN010 - GAGCCCGCACG-TACTGAGATTGGGGAGGAGAAATATTGCAGTCCGGAGC -2053

SEQIDN07 - GGTTACATTGGTAACCAGCATTTCGGGGGTATGTGGGTGGGAGACAACTC -2150
 | | | | | | | | | | | | | |
 SEQIDN010 - TACTCATCAGGTGGTATACTGGATCATTCCTTTGCCATGGCTTAGAAAC -2103

SEQIDN07 - TACTACATCAAACCTACATCCAAATGATGATTGCCAACAAATTAACATGA -2200
 | | | | | | | | | | | | | |
 SEQIDN010 - CACTACGTCAAGAAGGACAGGAAATGGTTCCAGGAACCATAACGCGTACCC -2153

SEQIDN07 - ATATGTCTTGCTTGCTCTCGTCGGCTCCGACATTGGAGGATTCACCTCA -2250
 | | | | | | | | | | | | | |
 SEQIDN010 - CAAGCATCTTGAAACCCATCCAGAGCTCGCAGATCAAGCATGGCTTTACA -2203

SEQIDN07 - TACGACAATGAGAA-TCAGCGAACGCCGTACCGGGGACTTGATGGTGA -2299
 | | | | | | | | | | | | | |
 SEQIDN010 - AATCTGTTCTAGAAATTTGCAGATACTGGGTAGAGCTAAGATATCCCTC -2253

SEQIDN07 - GGTATGTGCAGGCGGGCTGCCTGTTGCCGTGGTTCAGGAACCACTATGAT -2349
 | | | | | | | | | | | | | |
 SEQIDN010 - ATCCAGCTCCTTTACGACTGCATGTTCCAAAACGTGGTCGATGGTATGCC -2303

SEQIDN07 - AGGTGGATCGAGTCCAAGGACCAGGAAAGGACTACCAGGAGCTGTACAT -2399
 | | | | | | | | | | | | | |
 SEQIDN010 - ACTTGCCAGATCTATGCTCTTGACCGATACTGAGGATACGACCTTCTTCA -2353

SEQIDN07 - GTATCCGAATGAAATGGATACGTTGAGGAAGTTCGTTGAATCCGTTATC -2449
 | | | | | | | | | | | | | |
 SEQIDN010 - ATGAGAGCCAAAAGTTCCTCGATAACCAATATATGGCTGGTGACGACATC -2403

SEQIDN07 - GCTGGCAGGAAGTGTGTACACGGCCATGTACCAGAATGCGGCTTTCGGA -2499

|| | || | | | | | | | | | |
 SEQIDN010 - -CTTGTAGCACCCATCCTCCACAGCCGTAACGAGGTTCGGGAGAGAACA -2452

 SEQIDN07 - AAGCCGATTATCAAGGCTGCTTCGATGTACAATAACGACTCAAACGTTTCG -2549
 || | | || | | | | | | | | | |
 SEQIDN010 - GAGATGTCTATCTCCCTCTATTCCACACCTGGTACCC-CTCAAACCTTGAG -2501

 SEQIDN07 - CAGGGCGCAGAACGATCATTTCTTCTTGGTGGACATGATGGATATCGCA -2599
 | | | | | | | | | | | | | | |
 SEQIDN010 - ACCGTGGGACGATCAGGGAGTCGCTTTAGGGAATCCTGTGCAAGGTGGCA -2551

 SEQIDN07 - TTCTGTGCGCGCCTGTTGTGTGGGAGAATTCGACCGAACGGAATTGTAC -2649
 | | | | | | | | | | | | | | |
 SEQIDN010 - GCGTTATCAACTACACTGCCAGGATTGTTGCCCCAGAGGATTATAATCTC -2601

 SEQIDN07 - TTGCCCCGTCTGACCCAATGGTACAAATTCGGTCCCGACTTTGACACCAA -2699
 || | | | | | | | | | | | | | |
 SEQIDN010 - TTCCACAACGTGGTGCCGGTCTACATCAGAGAGGGTGCCATCATTCCGCA -2651

 SEQIDN07 - GCCTCTGGAAGGAGCGATGAACGGAGGGGACCGAATTACAACTACCCTG -2749
 || | | | | | | | | | | | | | |
 SEQIDN010 - AATTCAGGTACGCCAGTGGATTGGCGAAGGAGGGCCTAATCCCATCAAGT -2701

 SEQIDN07 - TACCGCAAAGTGAATCACCAATCTTCGTGAGAGAAGGTGCGATTCTCCCT -2799
 | | | | | | | | | | | | | | |
 SEQIDN010 - TCAATATCTACCCTGGAAGGACAAGGAGTATGTGACGTACCTTGATGAT -2751

 SEQIDN07 - ACCCGCTACACGTTGAACGGTGAAAACAAATCATTGAACACGTACACGGA -2849
 | | | | | | | | | | | | | | |
 SEQIDN010 - GGTGTTAGCCGCGATAGTGCACCAGATGACCTCCCGCAGTACCGCGAGGC -2801

 SEQIDN07 - CGAAGATCCGTTGGTGTGTTGAAGTATTCCCCCTCGGAAACAACCGTGCCG -2899
 | | | | | | | | | | | | | | |
 SEQIDN010 - CTATGAGCAAGCGAAGGTGCAAGGCAAAGACGTCCAGAAGCAACTTGCGG -2851

 SEQIDN07 - ACGGTATGTGTTATCTTGATGATGGCGGTGTGACCACCAATGCTGAAGAC -2949
 | | | | | | | | | | | | | | |
 SEQIDN010 - TCATTCAAGGGAATAAGACTAATGACTTCTCCGCTCCGGGATTGATAAG -2901

 SEQIDN07 - AATGGCAAGTTCTCTGTCGTCAAGGTGGCAGCGGAGCAGGATGGTGGTAC -2999
 | | || | | | | | | | | | | |
 SEQIDN010 - GAGGCAAAGGGTTATACCGCAAAGTTTCTATCAAACAGGAGTCAAAGA -2951

 SEQIDN07 - GGAGACGATAACGTTTACGAATGATTGCTATGAGTACGTTTTTCGGTGGAC -3049
 || | | | | | | | | | | | | | |
 SEQIDN010 - CAAGACCGTACTGTACCATGAGCCAAAACACAACGGATACGACCCCT -3001

 SEQIDN07 - CGTTCTACGTTTCGAGTGCGCGGCGCTCAGTCGCCGTCGAACATCCACGTG -3099
 | | | | | | | | | | | | | | |
 SEQIDN010 - CTAAGGAAGTTGGTAATTATTATACCATCATTCTTTGGTACGCACCGGGC -3051

 SEQIDN07 - TCTTCTGGAGCGGGTTCTCAGGACATGAAGGTGAGCTCTGCCACTTCCAG -3149
 | | | | | | | | | | | | | | |
 SEQIDN010 - TTTGACGGCAGCATCGTCGATGTGAGCCAGGCGACCGTGAACATCGAGGG -3101

SEQIDN07 - GGCTGCGCTGTTCAATGACGGGGAGAACGGTGATTCTGGGTTGACCAGG -3199
| | | | | | | | | | | |
SEQIDN010 - CGGGGTGGAATGCGAAATTTTCAAGAACACCGGCTT---GCATACGGTT -3147

SEQIDN07 - AGACAGATTCTCTGTGGCTGAAGTTGCCAACGTTGTTCTCCCGGACGCT -3249
| | | | | | | | | | | |
SEQIDN010 - GTAGTCAACGTGAAAGAGGTGATCGGTACCACAAAGTCCGTCAAGATCAC -3197

SEQIDN07 - GTGATCACAATTACCTAA -3267
| | | | | | | |
SEQIDN010 - TTG---CACTACCGCTTAG -3213

Identity : 1119 (34.83%)

Number of gaps inserted in SEQIDN07: 1

Number of gaps inserted in SEQIDN010: 21

===03-MAY-2001=====NALIGN=====PC/GENE===

==03-MAY-2001=====NALIGN=====PC/GENE==

* ALIGNMENT OF TWO NUCLEOTIDE SEQUENCES. *

The two sequences to be aligned are:

SEQIDN07.

Total number of bases: 3267.

SEQIDN011.

Total number of bases: 3279.

Open gap cost : 50

Unit gap cost : 20

The character to show that two aligned residues are identical is '|'

```
SEQIDN07 - ATGTTTTC AACCTT GCGTTT GTCGCACCTAGT GCGCTGGGAGCCAGTAC -50
          ||||| | |||| | || | || || || ||||| ||||| ||
SEQIDN011 - ATGTTTCCTACCCTGACCTTCATAGCGCCAGCGCGCTGGCCGCCAGCAC -50

SEQIDN07 - CTTCGTAGGGGCGGAGGTCAGGTCAAATGTTTCGTATCCATTCCGCTTTTC -100
          ||| || || ||||| || || || ||||| || ||||| ||
SEQIDN011 - CTTTGTGGGCGCGGATATCCGATCGGGCATTGCGATTCAATCCGCTCTTC -100

SEQIDN07 - CAGCTGTGCACACAGCTACTCGCAAAACCAATCGCCTCAATGTATCCATG -150
          || ||||| || |||| | || | ||||| ||||| ||
SEQIDN011 - CGGCCGTGCGCAACGCTGTGCGCAGGAGCAAACATTACAATGTATCCATG -150

SEQIDN07 - ACCGCATTGTCCGACAAACAAACGGCTACTGCGGGTAGTACAGACAATCC -200
          ||||| ||||| ||||| ||||| || || ||||| ||
SEQIDN011 - ACCGCATTGTCTGACAAGCAAACCGCTATCAGTATTGGCCCTGACAATCC -200

SEQIDN07 - GGACGGTATCGACTACAAGACCTACGATTACGTCGGAGTATGGGGTTTCA -250
          ||||| ||||| || ||||| || || || || || ||
SEQIDN011 - GGACGGTATCAACTACCAAACTACGATTACATCCCTGTAGCGGGCTTTA -250

SEQIDN07 - GCCCCCTCTCCAACACGAAGTGGTTTGCTGCCGGCTCTTCTACCCCGGGT -300
          ||||| ||||| ||||| ||||| || ||||| ||
SEQIDN011 - CGCCCCCTCTCCAACACCAACTGGTATGCTGCCGGCTCTTCCACTCCGGGC -300

SEQIDN07 - GGCATCACTGATTGGACGGCTACAATGAATGTCAACTTCGACCGTATCGA -350
          ||||| || ||||| ||||| ||||| ||||| || ||
SEQIDN011 - GGCATCACCGACTGGACCGCTACCATGAATGTCAAATTGACCGCATTGA -350

SEQIDN07 - CAATCCGTCCATCACTGTCCAGCATCCCGTTCAGGTTCAAGTACGTCAT -400
          ||||| || | |||| | |||| | ||||| ||||| ||
SEQIDN011 - CAATCCGTCTACTCCAATAACCATCCTGTTCAAGTTCAGGTCAGTTCGT -400

SEQIDN07 - ACAACAACAACAGCTACAGGGTTCGCTTCAACCCTGATGGCCCTATTCGT -450
          ||||| ||||| |||| | |||| | |||| | ||||| ||
SEQIDN011 - ACAACAACAACAGCTTCAGGATTCGCTTCAACCCTGATGGCCCCATTTCGT -450
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SEQIDN07 - GATGTGACTCGTGGGCCTATCCTCAAGCAGCAACTAGATTGGATTCTGAAC -500
|| || |||| || |||||||| || |||||||| ||||||||||||
SEQIDN011 - GACGTCTCTCGAGGACCTATCCTGAAACAGCAACTCACTTGGATTCTGAAA -500

SEQIDN07 - GCAGGAGCTGTGACAGGGGATGTGATCCCGGAATGACTTTACATCAGAAG -550
|||||||||| | |||||||| |||| |||| ||| | ||||
SEQIDN011 - CCAGGAGCTGGCGCAGGGATGTAATCCGAACATGAGCTTCTCTCTCTGAAG -550

SEQIDN07 - GTTCTTGACTTTTGAGACCAAGGATCTAAGCGTCATCATCTACGGAAAT -600
||||| | ||||| ||||| |||| |||| |||| ||||
SEQIDN011 - GTTTTTTGTCTTTTGAAACCAAGACCTAAACGTTATAATCTACGGCAAC -600

SEQIDN07 - TTCAAGACCAGAGTTACGAGAAAGTCTGACGGCAAGGTCATCATGGAAAA -650
| ||||| ||||| |||| ||| || ||||| || |||||||| ||
SEQIDN011 - TGCAAGATGAGAGTCACGAAGAAG---GATGGCTACCTCGTCATGGAGAA -647

SEQIDN07 - TGATGAAGTTGGAAGTGCATCGTCCGGGAACAAGTGCCGGGGATTGATGT -700
||| || | ||| || || ||||| | |||||||||
SEQIDN011 - TGACGAGTGCAACTCGCAATCAGATGGCAATAAGGTAGAGGATTGATGT -697

SEQIDN07 - TCGTTGATAGATTATACGGTAACGCTATCGTTCCGTCAACAAGAACTTC -750
|||||| | |||||||| |||| |||||||| | ||| ||
SEQIDN011 - ACGTTGACCGGTATACGGTAATGCTATTGCTTCCGTACAAACGAATTTT -747

SEQIDN07 - CGCAACGACGCGGTCAAGCAGGAGGGATTCTATGGTGCAGGTGAAGTCAA -800
| ||| ||| | | ||| |||||||||||||||||||||
SEQIDN011 - CACAAAGACACTTCTCGGAACGAGAAATTCTATGGTGCAGGTGAAGTCAA -797

SEQIDN07 - CTGTAAGTACCAGGAC-----ACCTACATCTTAGAACGCA -835
|||| || |||| |||| | |||||
SEQIDN011 - CTGTCGCTATGAGGAGCAGGTAAGGCGCCGACTTATGTTCTAGAACGCT -847

SEQIDN07 - CTGGAATCGCCATGACAAATTACAACCTACGATAACTGAACTATAACCAG -885
||||| |||||||| |||||||| ||||| |||||||| |||||
SEQIDN011 - CTGGACTCGCCATGACCAATTACAATTACGACAACCTGAACTACAACCAA -897

SEQIDN07 - TGGGACCTTAGACCTCCGCATCATGATGGTGCCTCAACCCAGACTATTA -935
||| | |||| | || || | ||| ||| ||
SEQIDN011 - CCAGACGTCGTTCTCCAGGTTATC-----CCGACCATCCCAACTACTA -941

SEQIDN07 - TATTCCAATGTACTACGCAGCACCTTGGTTGATCGTTAATGGATGCGCCG -985
|||||||||||||||||||||| ||||| |||| | |||||||||
SEQIDN011 - CATTCCAATGTACTACGCAGCACCGTGGTTGGTCGTTACGGGATGCGCGG -991

SEQIDN07 - GTACTTCGGAGCAGTACTCGTATGGATGGTTCATGGACAATGTCTCTCAA -1035
| || ||| |||| |||||||| || ||||| |||||||||||||
SEQIDN011 - GGACATCGAAGCAATACTCGTACGGTTGGTTTATGGACAATGTCTCTCAG -1041

SEQIDN07 - TCTTACATGAATACTGGAGATACTACCTGGAATTCTGGACAAGAGGACCT -1085
|| |||||||| |||||||||| | ||||| | ||||| || ||||
SEQIDN011 - TCGTACATGAACACTGGAGATACGGCGTGGAACTGCGGACAGGAAAACCT -1091

SEQIDN07 - GGCATACATGGGCGCGCAGTATGGACCATTGACCAACATTTGTTTACG -1135

SEQIDN011	-	GGCATACATGGGCGCGCAATACGGGCCATTGTGATCAGCACTTTGTGTATG	-1141
SEQIDN07	-	GTGCTGGGGGTGGGATGGAATGTGTGGTCACAGCGTTCTCTCTTCTACAA	-1185
SEQIDN011	-	GTGATGGAGATGGCCTTGAAGATGTCGTCAAAGCGTTCTCCTTTCTTCAA	-1191
SEQIDN07	-	GGCAAGGAGTTCGAGAACCAAGTTCTCAACAAACGTTCAAGTAATGCCTCC	-1235
SEQIDN011	-	GGAAAGGAGTTCGAAGACAAAAAAGTCAACAAGCGTTCTGTAATGCCTCC	-1241
SEQIDN07	-	GAAATACGTCTTTGGTTTCTTCCAGGGTGTTTTCGGGACTTCTTCCTTGT	-1285
SEQIDN011	-	GAAGTACGTGTTTGGTTTCTTCCAGGGTGTTTTCGGTGCACTTTCACTGT	-1291
SEQIDN07	-	TGAGAGCGCATATGCCAGCAGGTGAGAACAACATCTCAGTCGAAGAAATT	-1335
SEQIDN011	-	TGAAGCAGAATCTGCCTGCCGGAGAGAACAACATCTCAGTGCAAGAGATT	-1341
SEQIDN07	-	GTAGAAGGTTATCAAAACAACAATTTCCCTTTGAGGGGCTCGCTGTGGA	-1385
SEQIDN011	-	GTGGAGGGTTACCAGGATAACGACTACCCCTTTGAAGGGCTCGCGGTAGA	-1391
SEQIDN07	-	CGTGGATATGCAAGACAACCTTGCGGGTGTTACCCACGAAGGGCGAATTTT	-1435
SEQIDN011	-	TGTTGATATGCAAGATGATCTGCGAGTGTTACTACCAAACCGAATATT	-1441
SEQIDN07	-	GGACCGCAAACAGGGTGGGTACTGGCGGGGATCCAAACAACCGATCGGTT	-1485
SEQIDN011	-	GGTCGGCAAACATGGTAGGCGAAGGCGGTGATCCTAATAACAGATCAGTC	-1491
SEQIDN07	-	TTTGAATGGGCACATGACAAAGGCCTTGTTTGTGACACAAATATAACTTG	-1535
SEQIDN011	-	TTTGAATGGGCACATGACAGGGGCCTTGCTGTGACACGAACGTAACCTTG	-1541
SEQIDN07	-	CTTCTTGAGGAATGATAACGAGGGGCAAGACTACGAGGTCAATCAGACGT	-1585
SEQIDN011	-	CTTCTTGAGGAACGATAACAGTGGGAAACCATAACGAAGTGAATCAGACAT	-1591
SEQIDN07	-	TAAGGGAGAGGCAGTTGTACACGAAGAACGACTCCCTGACGGGTACGGAT	-1635
SEQIDN011	-	TGAGGGAGAAACAGTTGTATACGAAGAATGATTCCTTGAACAACACCGAT	-1641
SEQIDN07	-	TTTGAATGACCGACGACGGCCCCAGCGATGCGTACATCGGTCACTCTGGA	-1685
SEQIDN011	-	TTTGAACCTACCTCGGATGGGCCTGGCGATGCGTACATTGGACATTTGGA	-1691
SEQIDN07	-	CTATGGGGGTGGAGTAGAATGTGATGCACTTTTCCAGACTGGGGACGGC	-1735
SEQIDN011	-	CTATGGTGGTGGAGTGGAGTGTGATGCAATCTTCCAGACTGGGGTCGAC	-1741
SEQIDN07	-	CTGACGTGGCCGAATGGTGGGGAAATAACTATAAGAAACTGTTTCAGCATT	-1785
SEQIDN011	-	CAGACGTGGCTCAATGGTGGGGAGAAAAGTACAAGAAGCTGTTTCAGCATT	-1791

SEQIDN07 - GGTCTCGACTTCGTCTGGCAAGACATGACTGTTCCAGCAATGATGCCGCA -1835
 ||||| ||||| ||||| || ||||| || || ||||| |||||
 SEQIDN011 - GGTCTCGATTTCGTGTGGCAGGATATGACGGTACCTGCGATGATGCCGCA -1841

 SEQIDN07 - CAAAATTGGCGATGACATCAATGTGAAACCGGATGG-----GAATT -1876
 | | | | |||| | || | | | | | | | |
 SEQIDN011 - CCGACTCGGTGATGCTGTCAACAAAAATTCCGGTAGTTCGGCGCCGGGCT -1891

 SEQIDN07 - GGCCGAATGCGGACGATCCGTCCAATGGACAATACTGGAAGACGTAC -1926
 ||||| ||||| ||||| ||||| ||||| ||||| || ||
 SEQIDN011 - GGCCGAATGAGAACGATCCATCCAACGACGATACTGGAATCTTAT -1941

 SEQIDN07 - CATCCCCAAGTGCTTGTAAGTATGCGTTATGAGA---ATCATGGTCG -1973
 ||||| ||||| || || || ||||| |||| | ||||| |
 SEQIDN011 - CATCCGCAAGTGCTCGTGACCGACATGCGCTATGGTGCAGAGTATGGAAG -1991

 SEQIDN07 - GGAACCGATGGTCACTCAACGCAACATTCATGCGTATACACTGTGCGAGT -2023
 ||||| ||||| ||||| ||||| || || || || || || ||
 SEQIDN011 - GGAACCGATGGTGTCTCAACGCAACATTCACGCCTACACTCTTTGTGAAT -2041

 SEQIDN07 - CTACTAGGAAGGAAGGGATCGTGAAAACGCAGACACTCTAACGAAGTTC -2073
 |||| || || || || || || ||||| || || || |||||
 SEQIDN011 - CTACCAGACGGGAGGGAATTGTGGGAAACGCAGACAGTTGACCAAGTTC -2091

 SEQIDN07 - CGCCGTAGCTACATTATCAGTCGTGGTGGTTACATTGGTAACCAGCATTT -2123
 ||||| || ||||| || ||||| || ||||| ||||| |||||
 SEQIDN011 - CGCCGCAGTTACATCATCAGTCGAGGAGTTACATCGGTAACCAGCATTT -2141

 SEQIDN07 - CGGGGGTATGTGGGTGGGAGACAACTCTACTACATCAAACCTACATCCAAA -2173
 ||| || ||||| || ||||| | || || | ||||| |||||
 SEQIDN011 - CGGAGGGATGTGGGTGGGACAAACAGTGCCACAGAATCCTACCTCCAAA -2191

 SEQIDN07 - TGATGATTGCCAACAATATTAACATGAATATGTCTTGCTTGCTCTCGTC -2223
 ||||| | || |||| || ||||| ||||| || || || || ||
 SEQIDN011 - TGATGTTGGCGAACATTATCAACATGAATATGTCGTGCCTCCCGTAGTT -2241

 SEQIDN07 - GGCTCCGACATTGGAGGATTCACCTCATACGACAATGAGAATCAGCGAAC -2273
 ||||| || ||||| || ||||| || | || | | || ||
 SEQIDN011 - GGCTCTGATATTGGCGGGTTCACCCAGTACAATGATGCGGGCGACCCAAC -2291

 SEQIDN07 - GCCGTGTACCGGGGACTTGATGGTGAGGTATGTGCAGGCGGGCTGCCTGT -2323
 || || || || ||||| || | ||||| ||||| |||||
 SEQIDN011 - CCC-----CGAGGATTGATGGTAAGATTCGTGCAGGCTGGCTGTCTGC -2335

 SEQIDN07 - TGCCGTGGTTCAGGAACCACTATGATAGGTGGATCGAGTCCAAGGACCAC -2373
 | ||||| ||||| ||||| ||||| ||||| || |||||
 SEQIDN011 - TACCGTGGTTCAGAAACCACTATGACAGGTGGATTGAGTCCAAGAAGCAC -2385

 SEQIDN07 - GGAAAGGACTACCAGGAGCTGTACATGTATCCGAATGAAATGGATACGTT -2423
 || ||| | ||||| || ||||| || || ||||| |||||
 SEQIDN011 - GGGAAGAAATACCAGGAGTTATACATGTACCCGGGCAAAAGGATACGTT -2435

 SEQIDN07 - GAGGAAGTTCGTTGAATTCCGTTATCGCTGGCAGGAAGTGTGTACACGG -2473

SEQIDN011	-	GAAGAAAGTTCGTTGAATTCGCGCTACCGCTGGCAGGAGGTTTGTACACAG	-2485
SEQIDN07	-	CCATGTACCAGAAATGCGGCTTTCGGAAAGCCGATTATCAAGGCTGCTTCG	-2523
SEQIDN011	-	CCATGTACCAAAATGCTACCACTGGAGAGCCGATCATCAAGGCGGCGCCC	-2535
SEQIDN07	-	ATGTACAATAACGACTCAAACGTTTCGAGGGCGCAGAACGATCATTTCCCT	-2573
SEQIDN011	-	ATGTACAACAACGACGTCAACGTGTATAAATCGCAGAATGATCATTTCCCT	-2585
SEQIDN07	-	TCTTGGTGGACATGATGGATATCGCATTCTGTGCGCGCCTGTTGTGTGGG	-2623
SEQIDN011	-	TCTCGGTGGACATGACGGCTATCGTATTCTCTGCGCACCTGTTGTGCGCG	-2635
SEQIDN07	-	AGAATTCGACCGAACGCGAATTGTACTTGCCCGTGCTGACCCAATGGTAC	-2673
SEQIDN011	-	AAAATGCGACAAGTCGCGAAGTGTACCTGCCTGTGTATAGCAAGTGGTTC	-2685
SEQIDN07	-	AAATTCGGTCCCGACTTTGACACCAAGCCTCTGGAAGGAGCGATGAACGG	-2723
SEQIDN011	-	AAATTCGGACCGGACTTTGACACTAAGCCCTTGAAAAATGAGATTCAAGG	-2735
SEQIDN07	-	AGGGGACCGAATTTACAACCTACCCTGTACCGCAAAGTGAATACCAATCT	-2773
SEQIDN011	-	AGGTGAGACGCTTTATAATTACGCTGACCGCTGAACGATTGCGCGATAT	-2785
SEQIDN07	-	TCGTGAGAGAAGGTGCGATTCTCCCTACCGCTACACGTTGAACGGTGAA	-2823
SEQIDN011	-	TTGTGAGGGAAGGGACTATTCTTCCGACACGGTACACGCTGGACGGTGTG	-2835
SEQIDN07	-	AACAAATCATTGAACACGTACACGGACGAAGATCCGTTGGTGTGTTGAAGT	-2873
SEQIDN011	-	AACAAATCTATCAACACGTACACAGACAATGATCCGCTTGTATTGAGCT	-2885
SEQIDN07	-	ATTCCCCCTCGGAAACAACCGTGCCGACGGTATGTGTTATCTTGATGATG	-2923
SEQIDN011	-	GTTCCCTCTCGAAACAACCAAGGCGCATGGCTTGTCTATCATGATGATG	-2935
SEQIDN07	-	GCGGTGTGACCACCAATGCTGAAGACAATGGCAAGTTCTCTGTCGTCAAG	-2973
SEQIDN011	-	GCGGTGTCAACACCAACGCTGAAGACTTTGGCAAGTATTCTGTGATCAGT	-2985
SEQIDN07	-	GTGGCAGCGGAGCAGGATGGTGGTACGGAGACGATAACGTTTACGAATGA	-3023
SEQIDN011	-	GTGAAGGCCGCGCAGGAAGGTTCTCAAATGAGTGTCAAGTTTGACAATGA	-3035
SEQIDN07	-	TTGCTATGAGTACGTTTTTCGGTGGACCGTTCTACGTTGAGTGC GCGGCG	-3073
SEQIDN011	-	AGTTTATGAACACCAATGGGGAGCATCGTTCTATGTTGTCGTGTCGTAATA	-3085
SEQIDN07	-	CTCAGTCGCCGTCGAACATCCACGTGTCTTCTGGAGCGGGTTCTCAGGAC	-3123
SEQIDN011	-	TGGGTGCTCCGCTAACATCAACGTATCTTCTCAGATTGGTCAACAGGAC	-3135


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SEQIDN07 - ATGAAGGTGAGCTCTGCCACTTCCAGGGCTGCGCTGTTCAATGACGGGGA -3173
          ||| | ||||| | | ||||| ||||| | |
SEQIDN011 - ATGCAACAGAGCTCCGTGAGTTCCAGGGCGCAAATGTTCACTAGTGCTAA -3185

SEQIDN07 - GAACGGTGATTTCTGGGTTGACCAGGAGACAGATTCTCTGTGGCTGAAGT -3223
          | || | | ||||| ||||| || | || ||||| |||
SEQIDN011 - CGATGGCGAGTACTGGGTTGACCAGAGCACGAACTCGTTGTGGCTCAAGT -3235

SEQIDN07 - TGCCCAACGTTGTTCTCCCGGACGCTGTGATCACAATTACCTAA -3267
          |||| | ||| || ||||| ||||| || | |
SEQIDN011 - TGCCTGGTGCAGTTATCCAAGACGCTGCGATCACTGTTTCGTTGA -3279

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Identity : 2450 (74.99%)
Number of gaps inserted in SEQIDN07: 3
Number of gaps inserted in SEQIDN011: 3

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===03-MAY-2001=====NALIGN=====PC/GENE===

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===03-MAY-2001=====NALIGN=====PC/GENE===

* ALIGNMENT OF TWO NUCLEOTIDE SEQUENCES. *

The two sequences to be aligned are:

SEQIDN07.

Total number of bases: 3267.

SEQIDN012.

Total number of bases: 1712.

Open gap cost : 50

Unit gap cost : 20

The character to show that two aligned residues are identical is '|'

```
SEQIDN07 - ATGTTTCAACCCTTGC GTTTGTCGCACCTAGTGC GCTGGGAGCCAGTAC -50
          |||
SEQIDN012 - ATG----- -3

SEQIDN07 - CTTCGTAGGGCGGAGGTCAGGTCAAATGTTCTGTATCCATTCCGCTTTTC -100
SEQIDN012 - ----- -3

SEQIDN07 - CAGCTGTGCACACAGCTACTCGCAAAACCAATCGCCTCAATGTATCCATG -150
SEQIDN012 - ----- -3

SEQIDN07 - ACCGCATTGTCCGACAAACAAACGGCTACTGCGGGTAGTACAGACAATCC -200
SEQIDN012 - ----- -3

SEQIDN07 - GGACGGTATCGACTACAAGACCTACGATTACGTCGGAGTATGGGGTTTCA -250
SEQIDN012 - ----- -3

SEQIDN07 - GCCCCCTCTCCAACACGAACTGGTTTGCTGCCGGCTCTTCTACCCCGGGT -300
SEQIDN012 - ----- -3

SEQIDN07 - GGCATCACTGATTGGACGGCTACAATGAATGTCAACTTCGACCGTATCGA -350
SEQIDN012 - ----- -3

SEQIDN07 - CAATCCGTCCATCACTGTCCAGCATCCCGTTCAGGTTCAGGTCACGTCAT -400
SEQIDN012 - ----- -3

SEQIDN07 - ACAACAACAACAGCTACAGGGTTCGCTTCAACCCTGATGGCCCTATTCTG -450
SEQIDN012 - ----- -3
```

SEQIDN07 - GATGTGACTCGTGGGCCTATCCTCAAGCAGCAACTAGATTGGATTGCAAC -500

SEQIDN012 - ----- -3

SEQIDN07 - GCAGGAGCTGTCAGAGGGATGTGATCCCGAATGACTTTCACATCAGAAG -550

SEQIDN012 - ----- -3

SEQIDN07 - GTTCTTGACTTTTGAGACCAAGGATCTAAGCGTCATCATCTACGGAAAT -600

SEQIDN012 - ----- -3

SEQIDN07 - TTCAAGACCAGAGTTACGAGAAAGTCTGACGGCAAGGTCATCATGGAAAA -650

SEQIDN012 - ----- -3

SEQIDN07 - TGATGAAGTTGGAAGTGCATCGTCCGGGAACAAGTGCCGGGGATTGATGT -700

SEQIDN012 - ----- -3

SEQIDN07 - TCGTTGATAGATTATACGGTAACGCTATCGCTTCCGTCAACAAGAACTTC -750

SEQIDN012 - ----- -3

SEQIDN07 - CGCAACGACGCGGTCAAGCAGGAGGGATTCTATGGTGCAGGTGAAGTCAA -800

SEQIDN012 - ----- -3

SEQIDN07 - CTGTAAGTACCAGGACACCTACATCTTAGAACGCACTGGAATCGCCATGA -850

SEQIDN012 - -----A -4

SEQIDN07 - CAAATTACAACCTACGATAACTTGAAGTATAACCAGTGGGACCTTAGACCT -900

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SEQIDN012 - CAAACTATAATTATGACAATTTGAAGTACAATCAACCGGACCTCATCCCA -54

SEQIDN07 - CCGCATCATGATGGTGCCCTCAACCCAGACTATTATATTCCAATGTACTA -950

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SEQIDN012 - CCTGCCCATGATTCAG-----ATCCTGACTACTATATTCCGATGTACTT -98

SEQIDN07 - CGCAGCACCTTGGTTGATCGTTAATGGATGCGCCGGTACTTCGGAGCAGT -1000

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SEQIDN012 - TGCGGCACCATGGGTGATCGCACATGGATATCGTGGCACCAGCGACCAGT -148

SEQIDN07 - ACTCGTATGGATGGTTTCATGGACAATGTCTCTCAATCTTACATGAATACT -1050

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SEQIDN012 - ACTCTTATGGATGGTTTTTGGACAATGTATCCAGTCTACACAAACACT -198

SEQIDN07 - GGAGATACTACCTGGAATTCTGGACAAGAGGACCTGGCATACTAGGGCGC -1100

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SEQIDN012 - GGCGATGATGCATGG---GCTGGTCAGAAGGATTGGCGTACATGGGGGC -245

SEQIDN07 - GCAGTATGGACCAATTTGACCAACATTTTGTGTTACGGTGCTGGGGGTGGGA -1150

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 SEQIDN012 - ACAATGTGGGCCTTTCGATCAACATTTTGTGTATGAGGCTGGAGATGGAC -295

 SEQIDN07 - TGAATGTGTGGTCACAGCGTTCTCTTCTACAAGGCAAGGAGTTCGAG -1200
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 SEQIDN012 - TTGAAGACGTTGTGACCGCATTCTCTTATTGCAAGGCAAGGAATATGAG -345

 SEQIDN07 - AACCAAGTTCTCAACAAACGTTCAAGTAATGCCTCCGAAATACGTCTTTGG -1250
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 SEQIDN012 - AACCAGGGACTGAATATACGTTCTGCAATGCCTCCGAAGTACGTTTTCGG -395

 SEQIDN07 - TTTCTTCCAGGGTGTTCGCGGACTTCTTCCTTGTGAGAGCGCATATGC -1300
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 SEQIDN012 - ATTTTCCAAGGCGTATTCGAGCCACATCGCTGCTAAGGGACAACCTAC -445

 SEQIDN07 - CAGCAGGTGAGAACAACATCTCAGTCGAAGAAATTGTAGAAGGTTATCAA -1350
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 SEQIDN012 - CTGCCGGCGAGAACAACGTCTCTTGAAGAAATTGTTGAAGGATATCAA -495

 SEQIDN07 - AACACAATTTCCCTTTCGAGGGGCTCGCTGTGGACGTGGATATGCAAGA -1400
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 SEQIDN012 - AATCAGAACGTGCCATTGAAGGTCTTGCTGTGGATGTTGATATGCAAGA -545

 SEQIDN07 - CAACTTGCGGGTGTTCACCACGAAGGGCGAATTTTGGACCGCAAACAGGG -1450
 ||||| || ||||| || || || ||||| ||||| || ||
 SEQIDN012 - TGACTTGAGAGTGTTCACTACGAGACCAGCGTTTGGACGGCAAACAAGG -595

 SEQIDN07 - TGGGTACTGGCGGGGATCCAAACAACCGATCGGTTTTTGAATGGGCACAT -1500
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 SEQIDN012 - TGGGGGAAGGCGGTGATCCAAACAACAAGTCAGTGTTTGAGTGGGCACAT -645

 SEQIDN07 - GACAAAGGCCTTGTTCGAGACAAATATAACTTGCTTCCTGAGGAATGA -1550
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 SEQIDN012 - GACAGGGGCCTTGTCTGCCAGACGAATGTAACCTGCTTCTTGAAGAACGA -695

 SEQIDN07 - TAACGAGGGGCAAGACTACGAGGTCAATCAGACGTTAAGGGAGAGGCAGT -1600
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 SEQIDN012 - GAAAAA-----TCCTTACGAAGTGAATCAGTCATTGAGGGAGAAGCAGT -739

 SEQIDN07 - TGTACACGAAGAACGACTCCCTGACGGGTACGGATTTTGAATGACCGAC -1650
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 SEQIDN012 - TGTATACGAAGAGTGATTCTTGACAACATTGATTTTGAAGTACTCCA -789

 SEQIDN07 - GACGGCCCCAGCGATGCGTACATCGGTCTGACTATGGGGTGGAGT -1700
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 SEQIDN012 - GATGGGCCTAGCGATGCGTACATTGGACACTTAGACTACGGTGGTGGTGT -839

 SEQIDN07 - AGAATGTGATGCACTTTTCCAGACTGGGGACGGCCTGACGTGGCCGAAT -1750
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 SEQIDN012 - GGAGTGTGATGCACTATTCCAGACTGGGGTCGACCAGACGTGGCTCAAT -889

 SEQIDN07 - GGTGGGGAAATAACTATAAGAACTGTTTCAGCATTGGTCTCGACTTCGTC -1800
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 SEQIDN012 - GGTGGGGCGATAACTACAAGAACTATTTCAGCATTGGTCTCGATTTCGTC -939

SEQIDN07 - TGGCAAGACATGACTGTTCCAGCAATGATGCCGCACAAAATTGGCGATGA -1850
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 SEQIDN012 - TGGCAAGATATGACGGTACCTGCGATGATGCCGCACCGACTCGGTGACCC -989

 SEQIDN07 - CATCAATGTGAAACCGGATGGGAAT-----TGGCCGAATGCCGACG -1891
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 SEQIDN012 - TGTGGGCACAAAATTCCGGTGAGACGGCGCGGGCTGGCCGAATGATAAGG -1039

 SEQIDN07 - ATCCGTCCAATGGACAATACAACCTGGAAGACGTACCATCCCCAAGTGCTT -1941
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 SEQIDN012 - ATCCATCCAACGGACGATACAATTGGAAGTCTTACCATCCGCAAGTGCTC -1089

 SEQIDN07 - GTAAC TGATATGCGTTATGAGAATCATGGTCGGGAACCGATGGTCACTCA -1991
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 SEQIDN012 - GTGACTGACATGAGGTATGACGATTACGGAAGAGATCCCATTGTTACGCA -1139

 SEQIDN07 - ACGCAACATTTCATGCGTATACACTGTGCGAGTCTACTAGGAAGGAAGGGA -2041
 ||||| | |||| | | | | | | ||||| ||||| |
 SEQIDN012 - ACGCAATCTCCATGCCTACACTCTTGTGAGTCTACTAGGAGGAAGGCA -1189

 SEQIDN07 - TCGTGGAACCGCAGACACTCTAACGAAGTCCGCCGTAGCTACATTATC -2091
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 SEQIDN012 - TTGTTGGAACCGCAGATAGTCTGACGAAGTCCGCCGCAGCTATATTATC -1239

 SEQIDN07 - AGTCGTGGTGGTTACATTGGTAACCAGCATTTCCGGGGTATGTGGGTGGG -2141
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 SEQIDN012 - AGTCGTGGAGGCTACATCGGTAATCAGCACTTGGTGGGATGTGGGTAGG -1289

 SEQIDN07 - AGACAACTCTACTACATCAAACCTACATCCAAATGATGATTGCCAACATA -2191
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 SEQIDN012 - AGACAACTCTTCTACGGAAGACTACCTCGCAATGATGGTTATCAACGTTA -1339

 SEQIDN07 - TTAACATGAATATGTCTTGCTTGCCTCTCGTCGGCTCCGACATTGGAGGA -2241
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 SEQIDN012 - TCAACATGAACATGTCCGGTGTCGGCTCGTTGGTTCCGATATTGGAGGT -1389

 SEQIDN07 - TTCACCTCATACGACAATGAGAATCAGCGAACCCGTGTACCGGGGACTT -2291
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 SEQIDN012 - TTCACGGAGCATGACAA-----GAGAAACCCTGCACACCGGACTT -1430

 SEQIDN07 - GATGGTGAGGTATGTGCAGGCGGGCTGCCTGTTGCCGTGGTTCAGGAACC -2341
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 SEQIDN012 - GATGATGAGATTTGTGCAGGCTGGATGCTTGCTACCGTGGTTCAGGAACC -1480

 SEQIDN07 - ACTATGATAGGTGGATCGAGTCCAAGGACCACGGAAGGACTACCAGGAG -2391
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 SEQIDN012 - ACTACGATAGGTGGATCGAGAGCAAGAAACACGGAAGAACTACCAAGAG -1530

 SEQIDN07 - CTGTACATGTATCCGAATGAAATGGATACGTTGAGGAAGTTCGTTGAATT -2441
 ||||| || | | |||| | |||| | | | | | |
 SEQIDN012 - TTGTACATGTACCGCGACCACTGGACGCCTTGAGAAGTTTGTGGAAC -1580

 SEQIDN07 - CCGTTATCGCTGGCAGGAAGTGTGTACACGGCCATGTACCAGAATGCGG -2491

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SEQIDN012 - CCGCTATCGCTGGCAGGAAGTGTATACACAGCCATGTATCAGAATGCTT -1630

SEQIDN07  - CTTTCGGAAAGCCGATTATCAAGGCTGCTTCGATGTACAATAACGACTCA -2541
      ||| ||||| ||||| ||| || || ||||| |||||
SEQIDN012 - TGAACGGGAAGCCGATCATCAAAACGGTCTCCATGTACAACAACGATATG -1680

SEQIDN07  - AACGTTTCGAGGGCGCAGAACGATCATTTCTTCTTGGTGGACATGATGG -2591
      ||||| || ||||| || || |||||
SEQIDN012 - AACGTCAAAGATGCTCAGAATGACCACTTCCT -1712

SEQIDN07  - ATATCGCATTCTGTGCGCGCTGTTGTGTGGGAGAATTCGACCGAACGCG -2641

SEQIDN07  - AATTGTACTTGCCCGTGCTGACCCAATGGTACAAATTCGGTCCCGACTTT -2691

SEQIDN07  - GACACCAAGCCTCTGGAAGGAGCGATGAACGGAGGGGACCGAATTTACAA -2741

SEQIDN07  - CTACCCTGTACCGCAAAGTGAATCACCAATCTTCGTGAGAGAAGGTGCGA -2791

SEQIDN07  - TTCTCCCTACCGCTACACGTTGAACGGTGAAAACAAATCATTGAACACG -2841

SEQIDN07  - TACACGGACGAAGATCCGTTGGTGTTTGAAGTATTCCCCCTCGGAAACAA -2891

SEQIDN07  - CCGTGCCGACGGTATGTGTTATCTTGATGATGGCGGTGTGACCACCAATG -2941

SEQIDN07  - CTGAAGACAATGGCAAGTTCTCTGTCGTCAAGGTGGCAGCGGAGCAGGAT -2991

SEQIDN07  - GGTGGTACGGAGACGATAACGTTTACGAATGATTGCTATGAGTACGTTTT -3041

SEQIDN07  - CGGTGGACCGTTCTACGTTTCGAGTGCGCGGCGCTCAGTCGCCGTCGAACA -3091

SEQIDN07  - TCCACGTGTCTTCTGGAGCGGGTTCTCAGGACATGAAGGTGAGCTCTGCC -3141

SEQIDN07  - ACTTCCAGGGCTGCGCTGTTCAATGACGGGGAGAACGGTGATTCTGGGT -3191

SEQIDN07  - TGACCAGGAGACAGATTCTCTGTGGCTGAAGTTGCCCAACGTTGTTCTCC -3241

SEQIDN07  - CGGACGCTGTGATCACAATTACCTAA -3267

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Identity : 1272 (74.30%)

Number of gaps inserted in SEQIDN07: 1

Number of gaps inserted in SEQIDN012: 5

===03-MAY-2001=====NALIGN=====PC/GENE===